

APPENDIX

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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Bio

Search for

Show:

☐ 1: NP_599320. two-component sys...[gi:19551318] BLink, Domains, Links

LOCUS NP_599320 551 aa linear BCT 12-JAN-2004

DEFINITION two-component system sensory transduction histidine kinase
[Corynebacterium glutamicum ATCC 13032].

ACCESSION NP_599320

VERSION NP_599320.1 GI:19551318

DBSOURCE REFSEQ: accession NC_003450.2

KEYWORDS

SOURCE Corynebacterium glutamicum ATCC 13032

ORGANISM Corynebacterium glutamicum ATCC 13032

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1

AUTHORS Nakagawa, S.

TITLE Complete genomic sequence of Corynebacterium glutamicum ATCC 13032

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 551)

AUTHORS NCBI Genomes Project.

TITLE Direct Submission

JOURNAL Submitted (23-SEP-2002) National Center for Biotechnology

Information, NIH, Bethesda, MD 20894, USA

COMMENT

REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from NCgl0067.

Genome re-annotation resulted from the combination of the
Corynebacterium glutamicum complete genomes deposited in GenBank
Accession Numbers BA000036 and NC_003450. The first version of
NC_003450 was derived from AX000000. BA000036 has a single 'c'
insertion at position 2231350 compared to AX000000. First version
of NC_003450 was annotated by NCBI staff using the GenMark HMM
prediction program and BLAST analysis results. Cgl#### systematic
gene names were used but the same gene names were later re-used in
BA000036 record. To avoid the confusion in the the present record
NCgl#### refers to the new systematic gene name for the revised
version of the Corynebacterium glutamicum genome, whereas, Cgl###
refers to the corresponding gene in the Corynebacterium glutamicum
complete genome deposited at GenBank Accession Number BA000036.
Method: conceptual translation.

FEATURES

source

Location/Qualifiers

1..551

/organism="Corynebacterium glutamicum ATCC 13032"

/db_xref="taxon:196627"

Protein

1..551

/product="two-component system sensory transduction
histidine kinase"

/EC_number="2.7.3.-"

CDS

1..551

/locus_tag="NCgl0067"

/coded_by="NC_003450.2:70506..72161"

/note="similar to signal transduction histidine kinase
regulating citrate/malate metabolism"

/transl_table=11
/db_xref="GeneID:1021092"

ORIGIN

1 msvggswdwn fkevdiiirfa trilviqvav valvvaictg ifavlmmndqm kteaehtals
61 igrsvasnpq ireevaldtq tganpsaeel adgdiqavaq aanertgalf vvitdglgir
121 lshpdeerlg eqvstsfeaa mrgeetmawe tgtlgasara kvpifapdss vpvgevsvgl
181 erdsvysrlp mflaalalis vlgiligvgv amgmrrrwer vtlglqpeel vtlvqnqtav
241 idgidegvla lspngtigvh neqaqsmiga gpmsgrtlke lgldlgldgv vlhgqhpstv
301 ahngrilyld fhpvrsgdqd lgyvvtirdr tdielserl dsvrtmthal raqrhefanr
361 ihtatglida grvhdaaefl gdisrnggqs hpligsahln eafllssflst asisasekgv
421 slrinsdtli lgtvkdpedv atilgnlinn aidaavagea prwieltlmd dadtlvisva
481 dsgpgipegv dvfatatqig dsednerthg hgigklcra larshggdvw vidrgtedga
541 vfgvklpgvm e

//

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NCBI | NLM | NIH

Jan 12 2004 10:46:34



results of BLAST

BLASTP 2.2.7 [Jan-02-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1074192799-32432-13245777434.BLASTQ4

Query=

(551 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

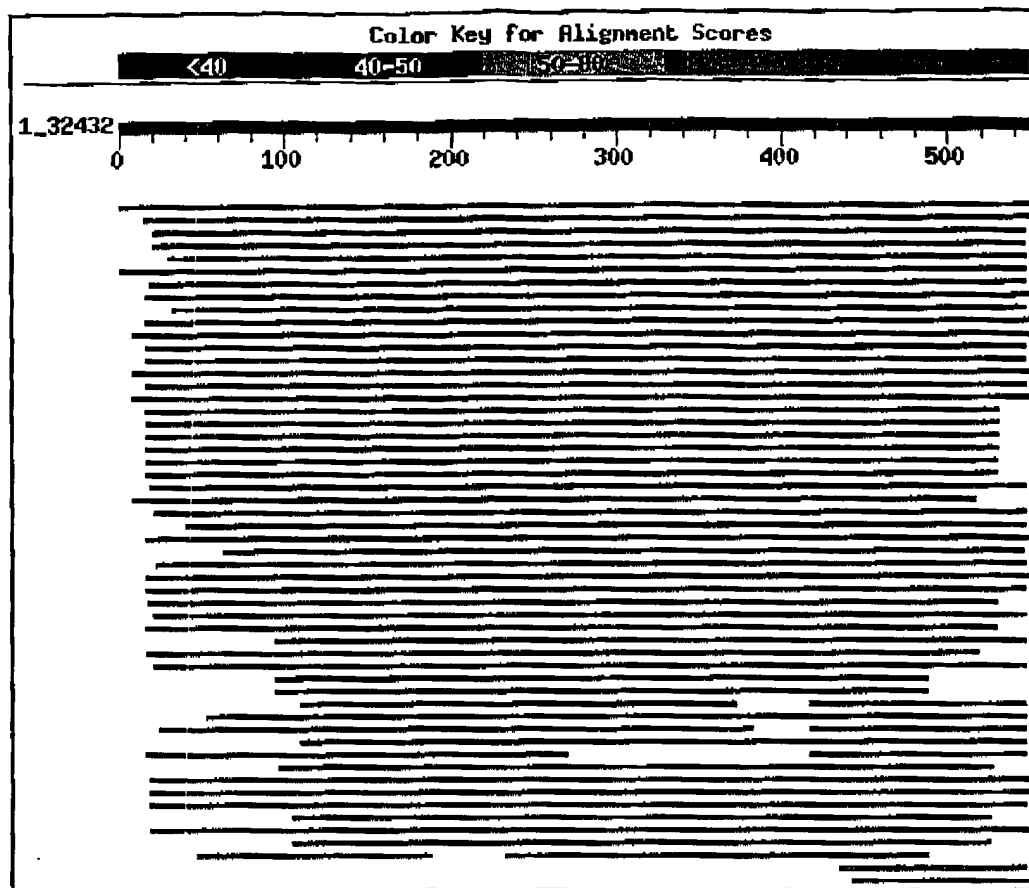
1,605,642 sequences; 528,039,549 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

Related Structures

Sequences producing significant alignments:

Score E
(bits) Value

gi 19551318 ref NP_599320.1	two-component system sensory t...	983	0.0
gi 25029461 ref NP_739515.1	putative sensor kinase [Coryne...	594	e-168
gi 21224173 ref NP_629952.1	putative two-component sensor ...	214	4e-54
gi 29828972 ref NP_823606.1	putative two-component system ...	213	1e-53
gi 15616401 ref NP_244706.1	two-component sensor histidine...	172	1e-41
gi 15640810 ref NP_230440.1	sensor kinase cita [Vibrio cho...	167	4e-40
gi 29829358 ref NP_823992.1	putative two-component system ...	162	2e-38
gi 21398877 ref NP_654862.1	HATPase_c, Histidine kinase-, ...	160	7e-38
gi 16080204 ref NP_391030.1	similar to two-component senso...	159	1e-37
gi 30019091 ref NP_830722.1	Two-component sensor kinase ci...	158	2e-37
gi 15800334 ref NP_286346.1	putative sensor-type protein [...	156	9e-37
gi 30260717 ref NP_843094.1	sensor histidine kinase [Bacil...	155	2e-36
gi 16767554 ref NP_463169.1	sensory histidine kinase [Salm...	154	4e-36
gi 16128602 ref NP_415152.1	putative sensor-type protein [...	153	7e-36
gi 16762986 ref NP_458603.1	two-component sensor kinase [S...	153	7e-36
gi 26246600 ref NP_752639.1	Sensor kinase dpiB [Escherichi...	153	9e-36
gi 15804717 ref NP_290758.1	putative 2-component sensor pr...	152	2e-35
gi 536970 gb AAA97025.1 ORF	f543 [Escherichia coli]	152	2e-35
gi 24115306 ref NP_709816.1	putative 2-component sensor pr...	152	2e-35
gi 27365978 ref NP_761506.1	signal transduction histidine ...	151	4e-35
gi 26250939 ref NP_756979.1	Sensor protein dcuS [Escherich...	151	4e-35

gi 37679787 ref NP 934396.1	putative sensor kinase Cita [V...	150	5e-35
gi 21223794 ref NP 629573.1	putative two-component sensor ...	149	1e-34
gi 2734636 gb AAC28951.1	histidine kinase [Escherichia coli]	148	2e-34
gi 15612960 ref NP 241263.1	two-component sensor histidine...	147	4e-34
gi 30018746 ref NP 830377.1	Two component system histidine...	147	7e-34
gi 16764002 ref NP 459617.1	sensory histidine kinase [Salm...	145	2e-33
gi 121219651 ref NP 625430.1	putative two component system ...	145	2e-33
gi 23100706 ref NP 694173.1	two-component sensor histidine...	144	5e-33
gi 16759585 ref NP 455202.1	sensor kinase DpiB [Salmonella...	144	5e-33
gi 28898486 ref NP 798091.1	putative sensor kinase Cita [V...	141	4e-32
gi 28211194 ref NP 782138.1	sensor kinase dpiB [Clostridiu...	140	8e-32
gi 23100675 ref NP 694142.1	two-component sensor histidine...	136	9e-31
gi 15641613 ref NP 231245.1	sensor kinase cita, putative [...	131	4e-29
gi 23112843 ref ZP 00098276.1	COG3290: Signal transduction...	131	4e-29
gi 18309513 ref NP 561447.1	two-component sensor histidine...	130	9e-29
gi 16077825 ref NP 388639.1	two-component sensor histidine...	128	3e-28
gi 21398531 ref NP 654516.1	HATPase_c, Histidine kinase-li...	127	8e-28
gi 30018763 ref NP 830394.1	Two-component sensor kinase yu...	125	2e-27
gi 23007702 ref ZP 00049454.1	COG3290: Signal transduction...	124	6e-27
gi 16077512 ref NP 388326.1	similar to two-component senso...	117	6e-25
gi 29375782 ref NP 814936.1	sensory box histidine kinase [...	116	9e-25
gi 15615315 ref NP 243618.1	two-component sensor histidine...	115	2e-24
gi 21398509 ref NP 654494.1	hypothetical protein predicted...	110	6e-23
gi 28900618 ref NP 800273.1	putative sensor kinase Cita [V...	110	7e-23
gi 29140597 ref NP 803939.1	sensor kinase Cita [Salmonella...	107	5e-22
gi 16759047 ref NP 454664.1	sensor kinase cita [Salmonella...	107	6e-22
gi 1705888 sp P52687 CITA KLEPN	Sensor kinase cita >gi 2126...	106	1e-21
gi 27366560 ref NP 762087.1	Signal transduction histidine ...	104	4e-21
gi 16763443 ref NP 459058.1	putative transcriptional regul...	103	1e-20
gi 37676272 ref NP 936668.1	putative sensor kinase Cita [V...	97	8e-19
gi 21219206 ref NP 624985.1	putative integral membrane sen...	94	6e-18
gi 21910305 ref NP 664573.1	putative two-component sensor ...	93	1e-17
gi 15675090 ref NP 269264.1	putative two-component sensor ...	92	3e-17
gi 19746058 ref NP 607194.1	putative two-component sensor ...	91	5e-17
gi 23121699 ref ZP 00103912.1	COG3290: Signal transduction...	89	2e-16
gi 22538059 ref NP 688910.1	sensor histidine kinase [Strep...	87	1e-15
gi 25011947 ref NP 736342.1	Unknown [Streptococcus agalact...	87	1e-15
gi 28894462 gb AAO61209.1	putative integral membrane senso...	85	3e-15
gi 29827327 ref NP 921961.1	putative membrane protein [Str...	80	8e-14
gi 29830694 ref NP 825328.1	hypothetical protein [Streptom...	72	3e-11
gi 37521385 ref NP 924762.1	two-component sensor histidine...	70	2e-10
gi 34810596 pdb 1OJG A	Chain A, Sensory Domain Of The Membr...	65	4e-09
gi 22968402 ref ZP 00015990.1	COG2200: FOG: ZAL domain [Rh...	64	1e-08
gi 33240571 ref NP 875513.1	Signal transduction histidine ...	63	2e-08
gi 16127201 ref NP 421765.1	sensory box histidine kinase/r...	62	3e-08
gi 17229920 ref NP 486468.1	two-component hybrid sensor an...	62	4e-08
gi 18450332 ref NP 569203.1	pli0050 [Listeria innocua] >gi...	61	6e-08
gi 22962960 ref ZP 00010566.1	COG0642: Signal transduction...	59	2e-07
gi 23040362 ref ZP 00071878.1	COG0642: Signal transduction...	59	2e-07
gi 399334055 ref NP 946331.1	sensor histidine kinase with a...	59	3e-07
gi 22987306 ref ZP 00032387.1	COG0784: FOG: CheY-like rece...	59	3e-07
gi 23125546 ref ZP 00107475.1	COG0784: FOG: CheY-like rece...	59	3e-07
gi 17231092 ref NP 487640.1	two-component sensor histidine...	59	3e-07
gi 33865287 ref NP 896846.1	two-component sensor histidine...	59	3e-07
gi 11362593 pir T50637	probable histidine kinase [imported...	59	3e-07
gi 20092217 ref NP 618292.1	sensory transduction histidine...	58	4e-07
gi 17548102 ref NP 521504.1	PROBABLE TWO-COMPONENT SENSOR ...	58	6e-07
gi 23473200 ref ZP 00128496.1	COG0642: Signal transduction...	57	7e-07
gi 28869841 ref NP 792460.1	bacteriophytochrome, putative ...	57	7e-07
gi 11497642 ref NP 069862.1	signal-transducing histidine k...	57	8e-07

gi 37523781 ref NP_927158.1	two-component hybrid sensor an...	57	1e-06
gi 18310298 ref NP_562232.1	two-component sensor histidine...	57	1e-06
gi 23471590 ref ZP_00126919.1	COG4251: Bacteriophytochrome...	56	1e-06
gi 38232698 ref NP_938465.1	Putative two-component system ...	56	1e-06
gi 22651420 gb AAL13332.1	bZIP histidine kinase [Pseudomon...	51	6e-05
gi 23109029 ref ZP_00095226.1	COG2202: FOG: PAS/PAC domain...	56	1e-06
gi 16125186 ref NP_419750.1	sensor histidine kinase/respon...	56	1e-06
gi 29829895 ref NP_824529.1	putative two-component system ...	56	1e-06
gi 23026365 ref ZP_00064851.1	COG2202: FOG: PAS/PAC domain...	56	2e-06
gi 15672378 ref NP_266552.1	sensor protein kinase [Lactoco...	56	2e-06
gi 37519945 ref NP_923322.1	two-component sensor histidine...	56	2e-06
gi 28199553 ref NP_779867.1	two-component system, sensor p...	56	2e-06
gi 23012921 ref ZP_00052899.1	COG0642: Signal transduction...	56	2e-06
gi 23127740 ref ZP_00109603.1	COG0642: Signal transduction...	56	2e-06
gi 25026835 ref NP_736889.1	putative sensor kinase [Coryne...	56	2e-06
gi 22995518 ref ZP_00039994.1	COG0642: Signal transduction...	56	2e-06
gi 23055901 ref ZP_00081977.1	COG0642: Signal transduction...	56	2e-06
gi 15836992 ref NP_297680.1	two-component system, sensor p...	56	2e-06
gi 22995932 ref ZP_00040213.1	COG0642: Signal transduction...	56	2e-06

Alignments

>gi|19551318|ref|NP_599320.1| two-component system sensory transduction histidine
[Corynebacterium glutamicum ATCC 13032]
gi|21322832|dbj|BAB97461.1| Two-component system, sensory transduction histidine
[Corynebacterium glutamicum ATCC 13032]
Length = 551

Score = 983 bits (2542), Expect = 0.0

Identities = 524/551 (95%), Positives = 524/551 (95%)

Query: 1 MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALS 60
MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALS
Sbjct: 1 MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALS 60

Query: 61 IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIR 120
IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIR
Sbjct: 61 IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIR 120

Query: 121 LSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF 180
LSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF
Sbjct: 121 LSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF 180

Query: 181 ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAV 240
ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAV
Sbjct: 181 ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAV 240

Query: 241 IDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETV 300
IDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKE HGQHPETV
Sbjct: 241 IDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKELGLDLGLDGVVLHGQHPETV 300

Query: 301 AHNGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANR 360
AHNGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANR
Sbjct: 301 AHNGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANR 360

Query: 361 IHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNXXXXXXXXXXXXXEXKGV 420
IHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNE BKGV
Sbjct: 361 IHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEAFLSSFLSTASISASEKGV 420

Query: 421 SLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVA 480
SLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVA
Sbjct: 421 SLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVA 480

Query: 481 DSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDEGA 540
DSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDEGA
Sbjct: 481 DSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDEGA 540

Query: 541 VFGVKLPGVME 551
VFGVKLPGVME
Sbjct: 541 VFGVKLPGVME 551

>gi|25029461|ref|NP_739515.1| putative sensor kinase [Corynebacterium efficiens YS-
gi|23494750|dbj|BAC19715.1| putative sensor kinase [Corynebacterium efficiens YS-
Length = 556

Score = 594 bits (1532), Expect = e-168
Identities = 332/538 (61%), Positives = 406/538 (75%), Gaps = 5/538 (0%)

Query: 16 IIRFATRILVIQVATVALVVAICTGIFAVLMMQMKTEAHTALSIGRSVASNPQIREEV 75
I+RFATRILVIQV TVA+VVA+C+ +F L ++Q+K EAE +ALSI R VA++PQ+R+EV
Sbjct: 3 IMRFATRILVIQVLTAVVVAVCSAVFTFLTVEQLKAEAEQSALSISRVAADPQVRDEV 62

Query: 76 ALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVST 135
A DT TGA P+A ELA G +Q A +A TGALF+VITDG GIRL+HPD++RLG+ VST
Sbjct: 63 ARDTFTGAEPATAELARGPLQEFHAQAQVSTGALFIVITDGNGIRLAHPDQQRLLGQVVST 122

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVPFAPDSSVPVGEVSVSGFERDSVYSRLPMFLAA 195
F+AA+RGEET+AWETGTLG SARAKVP+FAP ++ PVG VSVGFER SV+ RLP L
Sbjct: 123 GFDAALRGEETIAWETGTLGESARAKVPFAPGTTTPVGGVSVGFERASVFDRLPPLMT 182

Query: 196 LALISVLGILIGVGVAMGMRRRNRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+A +VL +++G GVA+ MRRRWE +TLGLQPEELV L++N TAV++G++EGVLAL P+G
Sbjct: 183 VAACAVLALILGAGVAVVMRRRWEITLGLQPEELVELLKNHTAVLNGVEEGVLALRPDG 242

Query: 256 TIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVR 315
TI VHN+QA+ + G ++GRTL E G P V+ N RILYLD HPV
Sbjct: 243 TIDVHNQQAREITGIEALAGRTLPELGMDEGIVDKLLRGDRPGAVSLNNRILYLDHPVT 302

Query: 316 RGDQDLGVVVTIADRTDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLIDAGRVDH 375
RGDQ+LG+V+TIRDRTD++EL+ERLDSVRTMT ALRAQRHEF+NRIHTATGLIDAGR HD
Sbjct: 303 RGDQELGHVITIRDRTDMVELTERLDSVRTMTQALRAQRHEFSNRIHTATGLIDAGRPHD 362

Query: 376 AAFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLILGTVK 435
AA FL I +GGQ HPL+G+ L E E+GV LRI DTLILG V
Sbjct: 363 AAFLRSIGGHGGQVHPLLGAELLEAFLLSSFITTAITASERGVGLRITDDTLILGEVD 422

Query: 436 DPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFAT 495
+ ED+AT+LGNL+ NAIDAA G+ PR ++LTL+DD DTLV++VAD+GPGI VDVFA
Sbjct: 423 NAEDIATVLGNLLTNAIDAAARGDEPRVDLTLLDDGDTLVMTVADTGPGITGDVDVFAA 482

Query: 496 ATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTE--DGAVFGVKLPGVME 550
+ D D HGHG+GLKL RALARS GGDVW+IDRG + GAVEG LPGVM
Sbjct: 483 PPVDDWTD--AIHGHGLGLKLSRALARSLGCDVWIIDRGGQPGSGAVFGASLPGVM 538

>gi|21224173|ref|NP_629952.1| putative two-component sensor [Streptomyces coelicolor
gi|7481675|pir|T35203 probable two-component sensor - Streptomyces coelicolor
gi|3036894|emb|CAA18527.1| putative two-component sensor [Streptomyces coelicolor
Length = 566

Score = 214 bits (545), Expect = 4e-54
Identities = 180/538 (33%), Positives = 269/538 (50%), Gaps = 37/538 (6%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASNPQIREEVALDTQ 80
+++L++Q+A A V + TG+F + DQ+ +A AL+I ++ A PQ+ ++
Sbjct: 30 SQVLLMQLAIAAGVAVLATGLFLAPLGDQLDDQAMRRALIAQTAAQPPQVVRDLRTTRP 89

Query: 81 TGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEEA 140
T A+G +Q A+ E T A +VV+ D G+R SH D ER+GE VST A
Sbjct: 90 T-----ANGFVQREAEVRVREATRAEYVVVMDRQGVVRSHTDPERIGEVVSTDPGQA 140

Query: 141 MRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALIS 200
+ G E M + GTLG SAR KVP+ D + VG VSVG DSV +RL + L +
Sbjct: 141 LAGREVMEIDDGTLGRSARGKVFLRDGDGEI-VGAVSVGIAYDSVRARLIHAIPGLFAYA 199

Query: 201 VLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVH 260
+ +G + + RR +R T L ++ L+ + A++ GI EGV+AL G + +
Sbjct: 200 GGALAVGALASWIISSRRVQRQTRDLAFSDIAGLLAEREAMLHGIREGVVALDRGGRVRL 259

Query: 261 NEQAQSMIG-AGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHPV----- 314
N++AQ ++G G GR+ E G+ + +A GR+ D V
Sbjct: 260 NDEAQRLLGIGGEAVGRSPDEALGA-----GRTADVLA--GRVTGTDLLTVRGQRV 308

Query: 315 ----RRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDA 370
R D G V T+RDRT++ +L LDS R + ALRAQ HE ANR+HT GL++
Sbjct: 309 LVANRMPTDDGGAVATLRDRTLEQLGRELDSTRGLIDALRAQDHEHANRMHTLLGLEL 368

Query: 371 GRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLI 430
DA EF+G++ + + I + +++ E+GV+LR++ T +
Sbjct: 369 EMYDDAVEFVGEVVGDRHVTAQI-TERIHDPLLAALLVGKATVAAERGVALRVSDRTRL 427

Query: 431 LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGV 490
+ DP + TI+GNL++NA+DAA AG A +E+ L + ++V D+GPGI
Sbjct: 428 PDRLVDPRLVTVGNLVDNALDAA-AGTAHARVEVELRAEGRAATLTVRDTCGPI--AA 484

Query: 491 DVFATATQIGDSEDNERTH-GHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
D G S H GIGL L R LA GG + GA F V LP
Sbjct: 485 DHRELVAAGWSTKEPPAHRERGIGLPLVRLAERQGGSA-TVGEAYGGGAEEFVVVLP 541

>gi|29828972|ref|NP_823606.1| putative two-component system sensor kinase [Strepto
avermitilis MA-4680]
gi|29606077|dbj|BAC70141.1| putative two-component system sensor kinase [Streptom
avermitilis MA-4680]
Length = 575

Score = 213 bits (541), Expect = 1e-53
Identities = 178/538 (33%), Positives = 275/538 (51%), Gaps = 37/538 (6%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASNPQIREEVALDTQ 80
+++L++QV+ A V + TG+F + Q+ +A AL+I ++ A+ PQI E+
Sbjct: 20 SQVLLMQVSIAGVAVLATGLFLAPLSAQLDDQAMRRALIAQTAAQPIAEDF----- 74

Query: 81 TGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEEA 140

PS G +Q A+ + +GA +VV+ + G+R SH D ++G+ VST A
Sbjct: 75 QATRPV---GGPVQTEAERIRKASGA EYVVVMNMDGVRWSHTDPTQIGKVVSTDPREA 130
Query: 141 MRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALIS 200
+ G++ M + CTLG SAR KVP+ D + VG VSVG E DSV +RL + + L +
Sbjct: 131 LAGKDVMQIDNGTLGRSARGKVPLRNADDKI-VGAVSVGIEYDSVRARLILAIPGLFAYA 189
Query: 201 VLGILIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVH 260
+ IG A + RR +R T L ++ L+ + A++ I EGV+AL G + +
Sbjct: 190 GAALAIGAVAAYLISRRVQRQTRDLAFSDISALLAEREAMLHSIREGVVALDRGGRVRL 249
Query: 261 NEQAQSMIGAGPMS-GRTLKXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVR---- 315
N++AQ ++G + G++L + G+ + +A GR+ D VR
Sbjct: 250 NDEAQRLLGLDAEAGQSLDDTLGP-----GRTTDVLA--GRVTGTDLLTVRGQRV 298
Query: 316 -----RGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDA 370
D G V T+RDRT++ +L LDS R + ALRAQ HE ANR+HT GL++
Sbjct: 299 LVANRMPTDDGGAVATLRDRTELEQLGRELDSTRGLIDALRAQDHEHANRMHTLLGLLEL 358
Query: 371 GRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLI 430
DA EF+G++ + + + + + E+GV+L I+ TL+
Sbjct: 359 DMYDDAVEFVGEVVGDRHTTAEQV-TEKIHDPLLAALLVGKATVAAERGVALWISDRTL 417
Query: 431 LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTMDADTLVISVADSGPGIPEGV 490
+ DP + T++GNL++NA+D AVAG +E+ L + T V+ V D+GPGIP V
Sbjct: 418 PDRLIDPRGLVTVGNLVDNALD-AVAGTPHARVEVELRAEGRTTVLRVRDTGPGIP--V 474
Query: 491 DVFATATQIGDSEDNERTHG-HGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ G + HG GIGL L R LA GG V D GA F V LP
Sbjct: 475 ERRELIFTDGTWKPPAHGKRGIGLSLVRRLAERQGG SARV-DEADGGGAFTVVLP 531

>gi|15616401|ref|NP_244706.1| two-component sensor histidine kinase [Bacillus halo
gi|21362444|sp|Q9RC53|CITS BACHD Sensor protein cits
gi|25298484|pir|G84129 two-component sensor histidine kinase cits [imported] - B
halodurans (strain C-125)
gi|5822800|dbj|BAA83946.1| CITS [Bacillus halodurans]
gi|10176464|dbj|BAB07558.1| two-component sensor histidine kinase [Bacillus halod
Length = 538

Score = 172 bits (437), Expect = 1e-41

Identities = 144/532 (27%), Positives = 260/532 (48%), Gaps = 33/532 (6%)

Query: 31 VALVVAICTGIFAVLMMDQ---MKTEAHTALSIGRSVASNPQIREVALDTQTGANPS 86
+AL++ + V + +Q ++ + ALS+ ++VA P++RE +
Sbjct: 18 IALLIIAMFVLLGVFLNEQYARTLEE QMGERALSVAQAVALIPELREAFS----- 67
Query: 87 AEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--STSFEAAMRGE 144
E D IQ +A++ TGA F+V+ + IR +HP ER+G+++ + A + GE
Sbjct: 68 -AERPDEIIQPIAESIRVETGASFIVVGNITDLIRYAHPLPERIGQRMVGGDNERALVHGE 126
Query: 145 ETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGI 204
++ G+LG S R KVP+F + + +G VSVG F + + + L A+ I V+ +
Sbjct: 127 SYVSKAVGSLGPSIRGKVPVFDNGKI-IGIVSVGFLMEDIQVIGERLIAMWQIVVVIM 185
Query: 205 LIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQA 264
++G+ + ++ TLGL+PEE+ Q + A++ I EGV+A++ G + + N+ A
Sbjct: 186 ILGLMGTWLVANTVKKATLGLPEEIGQQFQQKEAILQSIHEGVIAVNKEGKVTLFNQAA 245

Query: 265 QSMIG---AGPMSGRTLKEXXXXXXXXXXXXXX--HGQHPETVAHNGRILVLD FHPVRRGD 318
+ + GR + + GQ+ + + + ++ P+
Sbjct: 246 MKYVDPELDKEDVLGRHVTDLVKHTRLPEVLQVGKGQYDQELRIGDKQAVVNRVPFIYYDH 305

Query: 319 QDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAE 378
+ +G V T RDR +I +LSE L +V+ ALRAQ HEF+N+++T +G + G++ +A +
Sbjct: 306 EIVGAVATFRDRNEIKKLSEELTNVKNYADALRAQTHEFSNKLNTISGFLQLGKIDEAVD 365

Query: 379 FLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKEKGVSLRINSDTLILGTVKD-- 436
F+ R Q +N+ E G+ + I+ + +L +++
Sbjct: 366 FIOK-ERKIQQEWIHFFIERVNDPTVSAVLLGKISQAQELGIDVDIDPSSQLLTPLQERQ 424

Query: 437 PEDVATILGNLINNAIDAABA-GEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFAT 495
E + T++CNL+ NA DA +A G + I ++ D D + V D+GPGIP + +
Sbjct: 425 QELLVTMIGNLLENAPDALLASGIENKKIYTSFTDMGDDPIFEVEDNGPGIPP--QLMES 482

Query: 496 ATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTSOGAVFGVKLP 547
+ G S E TH G GL L + GG ++ ++ G GA F + +P
Sbjct: 483 IFEEGFST-KEGTH-RGFGLALVKKAVHELGGAI-F-LEEGELGGACFVLTIP 531

>gi|15640810|ref|NP_230440.1| sensor kinase cita [Vibrio cholerae O1 biovar eltor
gi|11277517|pir|C82280 sensor kinase cita VC0791 [imported] - Vibrio cholerae (N16961 serogroup O1)
gi|9655240|gb|AAF93956.1| sensor kinase cita [Vibrio cholerae O1 biovar eltor str
Length = 565

Score = 167 bits (424), Expect = 4e-40
Identities = 154/569 (27%), Positives = 255/569 (44%), Gaps = 44/569 (7%)

Query: 1 MSVGGSDWKNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALS 60
M + + + + K + F R+ + VA V + + + + G F + + + + AL
Sbjct: 1 MKISLAQLHTRKVCQTLSPQQRVGALLVAMVVIQLSLVAGFFHQTLSLQDQISTKALI 60

Query: 61 IGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVTIDGLGIR 120
R +A++P + + L Q N AE +QA + A F+VI D GIR
Sbjct: 61 QAREIATDPNL---IVLIQQ---NRLAE-----VQAKIDRLQRISDANFIVIGDANGIR 108

Query: 121 LSHPDEERLG--EQVSTSFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSV 178
++HPDE+++G Q S A GE + + G+LG + R K I AP + +G VSV
Sbjct: 109 IAHPEQKIGLPMQGGDSRRALKEGEYYTSTQKGS LGWAIRGKAAIVAPSGEI-LGVVSV 167

Query: 179 GFERDSVYSRLPMFLAALALISVLGILIGVGVMGMRRRWERVTLGLQPEELVTLVQNQT 238
G+ D++ S L ++ + +L +L+ A R ++ ++PEE+ + Q
Sbjct: 168 GYLLDNISSWLRVYSYPVIFTVLLMLLSALGAWIFTRHIKQMFNMEPEEIAMNLNLQQ 227

Query: 239 AVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGP---MSGRTLKEXXXXXXXXXXXXXXH- 293
+++ + EG++A+S G I N +A +++G + GR ++E
Sbjct: 228 SILQSVYEGIVAISLKGEILSVNAKALNILGLAHQPTHIGRNVQEFITPTCFMGASPF 287

Query: 294 -----GQHPETVAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVR 344
Q E ++ NG L + P+ G Q +G+VV+ R R D L+ +L +R
Sbjct: 288 GKLAQQNRVSQQDELISCNGETLVANRVPINSGQQQIGWVVSFRRRNDFNTLTSQLTQIR 347

Query: 345 TMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXX 404
LR HEFANR+ T GLI G +A + I R + LI
Sbjct: 348 QHNDNLRVMSHEFANRLSTIGGLIQIGAYDEAVK---TIRRETAEQQQLIDFIAQTFFHPK 404

Query: 405 XXXXXXXXXXXXXKEKGVSLRINSDTLILGTVKDPE-----DVATILGNLINNAIDAAG- 458

K + L + D L ++P+ ++A +LGNL++NA +A +
Sbjct: 405 VIAGLLLGKYSRAKELGLCLFDFPLS-HLHQEPQCMTSDELA AVLGNLLDNAFEATLKNP 463
Query: 459 EAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLK 518
+ + I L L D+ LVI VAD+G GI D+ T G S N+ GHGIGL L
Sbjct: 464 HSNKTIISLLTLDNGAELVIEVADNGIGI--SADIAQTLEFLKGVSSKNQ--EGHGIGLYLV 519
Query: 519 RALARSHGGDVWVIDRGTEGDGAVFGVKLP 547
G + +ID G +F + +P
Sbjct: 520 HQFVTQAHGSI-LIDSAEPQGTIFSIFIP 547

>gi|29829358|ref|NP_823992.1| putative two-component system sensor kinase [Strepto
avermitilis MA-4680]
gi|29606465|dbj|BAC70527.1| putative two-component system sensor kinase [Streptom
avermitilis MA-4680]
Length = 565

Score = 162 bits (409), Expect = 2e-38
Identities = 152/537 (28%), Positives = 248/537 (46%), Gaps = 27/537 (5%)

Query: 19 PATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVALD 78
A ++ +Q +A++VA V Q + A +++ RSVA P +R +
Sbjct: 12 LAGQLFAMQAVLIAVLVAGYALFTYVSDRSQAEEAARRQTMAVARSVADAPSVRAAIR- 70
Query: 79 TQTGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSE 138
++PSA +Q A TG FV I + GIR +HP+ + +GE+
Sbjct: 71 ----SDPSAA-----LQPYALQVQRHTGVDFVTIMNPRGIRWTHPNPDLIGERFLGHTT 120
Query: 139 AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALAL 198
A++GE TGTLG S RA PI D + +G VS G + +++ R+ + AL
Sbjct: 121 RALKGESFTETYTGTLGPSVRAVTPI--RDGTRIIGLVSAIKVEAITKRVDQVOTALIG 178
Query: 199 ISVLGILIGVGVAMGMRRRWERVTGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIG 258
++ + +G + R R T G+ EL + A + + EG+L L +
Sbjct: 179 VAAGALTGGIGTYVINARLRRSTHGMNAEELSRMHDYHQAALHAVREGLLMLDGGQFRVA 238
Query: 259 VHNEQAQSMIG-AGFMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAH--NGRILYLPFHPVR 315
+ N+ + ++G G + GR++ E + H R+L ++ PV
Sbjct: 239 LINDGGRELLGVTGDIVGRSVAELGLPAALTGALLSAEPRVDEVHLTAARVLVNTSPVS 298
Query: 316 RGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVD 375
G++ G VVT+RD T++ L LDS R T ALR+Q HE ANR+HT LI+ GR +
Sbjct: 299 GGERR-GTVVTLRDVTELQSLMGELDSERGFTTALRSQAHEAANRLHTTVVSLIELGRAEE 357
Query: 376 AAEF-LGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKGVSLRINSDTLILGTV 434
A +F ++ + ++ + ++E E+GV L ++ ++ + +
Sbjct: 358 AVDFATAELELAQALTDHVVSAA--VSEPVLALLLGKAAQANERGVELLVSEESALDDGL 415
Query: 435 KDP---EDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGV 490
P D+ TILGNLI+NA+DAA R + +T+ DA LV+ VAD+G G+
Sbjct: 416 LPPSLPARDLVITILGNLIDNAVDAAQGS MRAR-VTVTVFTDASGLVLRVADTGAGVDPAY 474
Query: 491 DVFATATQIGDSEDNERTHGHGIGLKLRLALARSHGGDVWVIDRGTEGDGAVFGVKLP 547
A + ++ + G G+GL L R H G + V + GA F V+LP
Sbjct: 475 -AEAVFQRGWSTKPATASGGRGLGLALVRQAVARHEGKLTVAE-ADGGGAEEFVRLP 529

>gi|21398877|ref|NP_654862.1| HATPase_c, Histidine kinase-, DNA gyrase B-, phytoch
ATPase [Bacillus anthracis A2012]
gi|30261052|ref|NP_843429.1| sensor histidine kinase [Bacillus anthracis str. Ame
gi|30254666|gb|AAP24915.1| sensor histidine kinase [Bacillus anthracis str. Ames]
Length = 529

Score = 160 bits (405), Expect = 7e-38
Identities = 141/543 (25%), Positives = 244/543 (44%), Gaps = 33/543 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMDQMKEAHTALSIGRSVASNPQIREEVA 76
+ T+I+ + +A+ VV+ GIF+ K+ E AL +S++ P I+E A
Sbjct: 7 VSLQTKIVSLIILFVVLALLAGIFVYIQSVDTKROVEQLALQTAKSLSFMPAIKE--A 64

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVST- 135
N +IQ++A+ E+ GA +V++ D G+ SH + E +G + +
Sbjct: 65 FQNNHKN-----NIQSIAEQVREQAGADYVIVEDRYGVMSHNSNELIGTKNNNP 115

Query: 136 -SFEAAMRGEETMAWETGTLGASARAKVPIFAP--DSSVPVGEVSVGFERDSVYSRLMP 192
++EA G GT + AK PI D VG V+V F + S +
Sbjct: 116 YNYEALTFGGYTYLEGNGTSSPALMAKAPIIVHNGDYDQVVGVTVEFLIKGIESNILSR 175

Query: 193 LAALALISVLGILIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252
+ L S+ +L+G+ + + R + TLGL+P E+ L + ++A++ I EG++A+
Sbjct: 176 TKEIILFSLAVLLVGIVGGILLARSIRKDTLGLSPNEIAALYRERSAILLSIKEGIIAID 235

Query: 253 PNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHG-QHPETVAHNGRILYLD 311
NG I + N A+ M+ ++G +++ ++ + +A ++ L+
Sbjct: 236 RNGFITMTNTSAEEMLH--VNGDYMQQHISKVLPEFHMervLENDQEIAPQDKVFILNM 292

Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
P+ + +G V + RD+T++ L + VR + LRAQ HEF N++ +GL+ G
Sbjct: 293 TPILENNNTVGVCVCSFRDKTELQNLVNTISEVRKYSIDLRAQTHEFTNKLFVLSGLLQLG 352

Query: 372 RVHDAAEFLGDISR-NGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLI 430
+A EF+ S + Q+H L H + EK + I D+
Sbjct: 353 HYREAIEFIQESNIHQSNHILFHQIH--DAKVQAILLGKIGTASEKKIDPFHIEGDS-A 409

Query: 431 LGTVKQPEDVA---TILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIP 487
L + D V+ TILGN+I+NA D AV+ + + + D +V V D G GIP
Sbjct: 410 LHPLPDHIKVSHLITILGNIIDNAFD-AVSEEREKNVSFFVTDIGHDIVFEVIDRGIGIP 468

Query: 488 EGVDFVATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547
+ T Q G S + + G GL + + G + I GA+F + LP
Sbjct: 469 --AEKITTFQKGFSS--TKGNNGYGLANVKEMVDVLEGTI-EIQNERNGGAIFTIYLP 522

Query: 548 GVM 550
+
Sbjct: 523 KTL 525

>gi|16080204|ref|NP_391030.1| similar to two-component sensor histidine kinase [Yu
subtilis]
gi|7428875|pir|A70009 two-component sensor histidine kinase homolog yufL - Bacil
subtilis
gi|1934809|emb|CAP07946.1| unknown [Bacillus subtilis]
gi|2635648|emb|CAP15141.1| yufL [Bacillus subtilis subsp. subtilis str. 168]
Length = 533

Score = 159 bits (402), Expect = 1e-37

Identities = 133/529 (25%), Positives = 245/528 (46%), Gaps = 27/528 (5%)

Query: 33 LVVAICTGIFAVLMDQMKEAHTALSIGRSVASNPQIREVALDTQTGANPSAEELAD 92
L + +C + L++ A+ T + A+ Q E VA T A + +
Sbjct: 11 LTIFVCIVVLIALLITFTVGAQTTKRIRDQEKATALQTAEMVAEAPMTAAALESKG-KQ 69

Query: 93 GDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEA-AMRGEETMAWET 151
++Q+ + + TG FVV+ D GIR +HPD ++G++ E+ ++G ++ +
Sbjct: 70 KELQSYTKRVQKITGTEFVVVMDMNGIRKTHPDPSKIGKKFRGGDESEVLKGVHISTAS 129

Query: 152 GTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVA 211
GTLG S RA VP++A + VG V+VG + + + L L I + I +GV A
Sbjct: 130 GTLGKSQRAFVPVYAENGK-QVGAVAVGITVNEIDEVISHSLRPLYFIICVSIFVGVIGA 188

Query: 212 MGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSM---- 267
+ + R + + GL+P E+ TL++ ++A+++ EG+LA+ +G I + N +A+ +
Sbjct: 189 VIVARTVKNIMYCLEPYEATLLEERSAMLESTKEGILAVDEHGKIKLANAEAKRLFVKM 248

Query: 268 -IGAGPMSGRTLKEXXXXXXXXXXXXXXHGQHP--ETVAHNGRILYLDHFVRRGDQDLGY 323
I P+ + + P V NG L + P++ Q +G
Sbjct: 249 GINTNPIDQDV--DDILPKSRLKKVIETKKPLQDRDVRINGLGLVFNVPVPIQLKGQTVGA 306

Query: 324 VVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFLGDI 383
+ T RD+T++ L+E+L V+ +ALRAQ HEF N++H GL+ D +++ DI
Sbjct: 307 IATFRDKTEVKHLAEQLSGVKMYANALRAQSHEFTMNLHVILGLVQLKEYDDLGDYIKDI 366

Query: 384 S-RNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLILGTVKDP---ED 439
+ + ++ +I + E+G +L I + +I DP +
Sbjct: 367 AIQQKSETSEIIND--VKSSVLGFLGKQSFIREQGANLDIECNGVI-PNAADPSVIHE 423

Query: 440 VATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQI 499
+ TI+GNLNN +D AVA + I +++ L I + D+G G+ E ++
Sbjct: 424 LITIIGNLINNGLD-AVADMPKKQITMSMRFHNSILDIBITDTGAGMSE-----EDQAKV 477

Query: 500 GDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547
+ + + G GL + + G + ++ +G F +++P
Sbjct: 478 FEQGYSTKGXNRGFGLYFTQQSIENLKQGM-ILTSEKNEGTTFSIRIP 524

>gi|30019091|ref|NP_830722.1| Two-component sensor kinase citS [Bacillus cereus AT
gi|29894634|gb|AAP07923.1| Two-component sensor kinase citS [Bacillus cereus ATCC
Length = 538

Score = 158 bits (400), Expect = 2e-37

Identities = 141/543 (25%), Positives = 238/543 (43%), Gaps = 31/543 (5%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMDQMKEAHTALSIGRSVASNPQIREEVA 76
+ T+I+ + + + VV + GIF + K + E AL +S++ P I+E
Sbjct: 7 VSLQTKIVSLIITLILFVLLLAGIFVYIQSVDTKHQVEQLALQTAKSLSFMPAIKEAF- 65

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVST- 135
Q + S IQ++A+ E+ GA +V++ D G+ SH + E +G + +
Sbjct: 66 ---QNNHKKST-----IQSIAEQVREQAGADYVIVEDRYGVMYSHSNSELIGTKSNNP 115

Query: 136 -SFEAAMRGEETMAWETGTLGASARAKVPIFAP--DSSVPVGEVSVGFERDSVYSRLPMF 192
++EA G GT G + AK PI D VG V+V F + S +
Sbjct: 116 YNYEALTFGGYYTLEGNGTSGPALMAKAPIIVHNGDYDQVVGVTVEFLIKGIESNILSR 175

Query: 193 LAALALISVLGILIGVGVAAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252

+ L S+ +L G+ + + R + TLGL+P E+ I + ++A++ I EG++A+
Sbjct: 176 TKEIILFSLGVLLAGIVGGILLARSIRKDTLGLPEPNEIAALYRERSAILLSIKEGIIAID 235
Query: 253 PNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXHCQHPETVAHNGRILYLDHFH 312
NG I + N A+ M+ + + + A ++ L+
Sbjct: 236 QNGFITMMNTSAERMLHVN--DDYMQQHISKVLPNFMERVLETDQEIAFQDKVFILNMT 293
Query: 313 PVRGQDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGR 372
P+ + +G V + RD+T++ L + VR + LRAQ HEF N++ +GL+ G+
Sbjct: 294 PILENNSTVGVCVCSFRDKTELQNLVNTISEVRKYSEDLRAQTHEFTNKLFVLSGLLQLGQ 353
Query: 373 VHDAAEFLGDISR-NGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKEGVSLRNSDTLIL 431
+A EF+ S + Q+H L H + EK + I D+ L
Sbjct: 354 YKEAIEFIQESNIHQSNHILFHQIH--DAKVQAILLGKIGTASEKKIDFHIEGDS-AL 410
Query: 432 GTVKDPEDVA---TILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
+ D V+ TILGN+I+NA D AV+ + + + D +V V DSG GIP
Sbjct: 411 HPLPDHIKVSHLITILGNIIDNAFD-AVSEREKSVSFFVTDIGRDI VFEVIDSGIGIPA 469
Query: 489 GVDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLPG 548
T I + + G GL + + CG + I GA+F + LP
Sbjct: 470 -----EKITTIFRKGFSTKGTDRGYGLANMKEMVDLLGGTI-EIQNEKNGGAIFTIYLPK 523
Query: 549 VME 551
+E
Sbjct: 524 NIE 526

>gi|15800334|ref|NP_286346.1| putative sensor-type protein [Escherichia coli O157:
gi|15829912|ref|NP_308685.1| putative sensor-type protein [Escherichia coli O157:
gi|25298480|pir|B90711| probable sensor-type protein [imported] - Escherichia col
O157:H7, substrain RIMD 0509952)
gi|25298485|pir|F95561| probable sensor-type protein cita [imported] - Escherichi
(strain O157:H7, substrain EDL933)
gi|12513518|gb|AAG54954.1| putative sensor-type protein [Escherichia coli O157:H7
gi|13360116|dbj|BAB34081.1| putative sensor-type protein [Escherichia coli O157:H
Length = 552

Score = 156 bits (395), Expect = 9e-37
Identities = 146/559 (26%), Positives = 246/559 (44%), Gaps = 44/559 (7%)

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASN 68
K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 8 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYLT LHVRDMAMNQAKIIASN 67
Query: 69 PQIREEVALDTQTGANPSABELADGDIQAVAQAANE---RTGALFVVITDGLGIRLSHPD 125
+ EV D + +A AN+ T +VVI D IRL HF+
Sbjct: 68 DSVISEVKTR-----DYKRLATIANKLQRDTDFDYVVIGDRHSIRLYHPN 112
Query: 126 EERLGEQVSTSFEEAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDS 184
E++G + + + A+ +GE G++G + RAK PIF D V +G VS+G+
Sbjct: 113 PEKICYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTPIFDDDGKV-IGVVSIGYLVSK 171
Query: 185 VYSRLPMFLAALA--LISVLGILIGVGAMGMRRRWERTLGLQPEELVTLVQNQTAVID 242
+ S FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+
Sbjct: 172 IDSWRAEFLLPMAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQQEALFS 229
Query: 243 GIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXXHCQHP 298
+ EG++A+ P+G I N A+ M+G G+ + E + +

Sbjct: 230 SVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIAEVVRPADFFTEQIDEKRQD 289
Query: 299 TVAH-NGRILYLDHFVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEF 357
VA+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE
Sbjct: 290 VVANFNGLSVIANREAIRSGDDLLGAIISFRSKDEISTLNAQLTQIKQYVESLRTL RHEH 349
Query: 358 ANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXXXX 415
N + T GL+ ++ + L + LI S +
Sbjct: 350 LNMWSTLNGLL---QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRQVAGLLFGKVQRA 406
Query: 416 XEKGVSRLI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDA 472
E G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+
Sbjct: 407 RELGLKMIIVPGSQLSGLPPGLDSTEFAAIVGNLLDNAFEASLRSDEGNKIVELFLSDEG 466
Query: 473 DTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARLSHGSDVW 530
D +VI VAD G G+PE + +F E E HGIGL L + GG V
Sbjct: 467 DDVVIEWADQCGVPESLRDKIFEQGVSTRADEPGE----HGIGLYLIASVYTRCGG-VI 521
Query: 531 VIDRGTEGAVFGVKLPV 549
++ G +F + +P V
Sbjct: 522 TLEDNDPCGTLFSIYIPKV 540

>gi|30260717|ref|NP_843094.1| sensor histidine kinase [Bacillus anthracis str. Ames]
gi|30254085|gb|AAP24580.1| sensor histidine kinase [Bacillus anthracis str. Ames]
Length = 536

Score = 155 bits (391), Expect = 2e-36
Identities = 133/543 (24%), Positives = 256/543 (47%), Gaps = 32/543 (5%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++ RI + A + +V+ + + +F ++ + ++ + AL + ++VA+ P+I+E A
Sbjct: 8 LKLQPRITLTISALILVVLMLTSYLFYYILSETVBEQIGKRALHVAKTVAAIPEIKE--A 65
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134
T+ NP++ IQ +A+ T A F+V+ + GIR +HP+ +++GE +
Sbjct: 66 FQTE---NPAS-----IIQPIAERIRMDTEADFI VVGNKEGIRYAHPERDKIGEAMIGG 116
Query: 135 TSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
+ + G+ ++ TG+LG S R KVPI ++ + +G VSVGF D ++ + ++
Sbjct: 117 DNKGVLLGKSYVSKATGSLGPSLRGKVPIRNOENI-IGVVS VGFMSDDIHGAVEVYVK 175
Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
+ I+++G+LIGV ++ + +R+ G++PEE+ +L + + VI + EG++ + N
Sbjct: 176 RVFWITIIIGLLIGVIGSIYLAGSIKRMFMGEPEEISSLYEEHSTVIQSVREGIIVIDQN 235
Query: 255 GTIGVHNEQAQSMIGAGPMS---GRTLKEXXXXXXXXXXXXXXHC--QHPETVAHNGRILYL 309
G I + N+ A ++ G + + G Q + G+ +
Sbjct: 236 GMISLVNQAAVDILALDEQRNIIGEFILDIIPNSTILDVLQTGEEQFDRQLNIKQAVIA 295
Query: 310 DFHFVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ P++ ++ G V ++R +++ +L+ L + T ALRAQ HE+ N ++T +GLI
Sbjct: 296 NRLPIKVIONKVTGVVSSRLKSEMDQLTAE LSQTKQYTEALRAQTHEYNNLLYTL SGLIQ 355
Query: 370 AGRVHDAAEFLGDISRNGGQSHPLIG--SAHLNEXXXXXXXXXXXXXXXXXXKEGVSRLNSD 427
DA E I + + + E + ++ +
Sbjct: 356 LELYEDALEL---IHKETAVYQDFVQFIMKRIQNPWLGGILIGFYNRARELKIEFMLDRE 412
Query: 428 TLI--LGTVKDPEDVATILGNLINNAIDAAVAGEA-PRWIELTLMDDADTLVISVADSGP 484

+ + L + V +ILGNLI NA +A E + + + + D + +VI V DSG
Sbjct: 413 SSLDKLSPPIESNYVVSILGNLITNAFEAIERNEEHDKKVRMFVTDIGEEIVIEVEDSGQ 472
Query: 485 GIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLSEHGDDVWVIDRGTEGAVFGV 544
GI + V E +R G GL + L G + I++G GA+F +
Sbjct: 473 GIHDEVITSIFYKGFSTKEGEKR---GYGLAKVKELVEDLNGSI-AIEKGDLCGALFII 527
Query: 545 KLP 547
LP
Sbjct: 528 ALP 530

>gi|16767554|ref|NP_463169.1| sensory histidine kinase [Salmonella typhimurium LT2]
gi|16422866|gb|AA123128.1| sensory histidine kinase in two-component regulatory
DcuR [Salmonella typhimurium LT2]
Length = 543

Score = 154 bits (390), Expect = 4e-36
Identities = 143/547 (26%), Positives = 254/547 (46%), Gaps = 42/547 (7%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVA 76
++ T ++++ A + V+ + I+ + + AL++ RS+A +P +RE +
Sbjct: 15 MKLGTTVILMVSAVLFVSVLVVHLYFSQISSMTRDALADKALAVARSLADSPAVREGLK 74
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
P AE IQ +A+A ++ G LF+V+T+ GIR SHP+ +R+G+
Sbjct: 75 -----KPPAES----GIQTLAEAVSQHNGFLFIVVTNMQGIRYSHPETQRIGQPFKGD 123
Query: 136 SFEEAMRGEBTMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A++G+E +A G L + R P++ + +G V++G E V ++ +
Sbjct: 124 DILLALQKENVAINRGFLAKALRVFTPVY-DEHHRQIGVVAIGLELSHVTQQINNSRGS 182
Query: 196 LALISVLGILIGVGVMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G L+G+ + + +R+ GL+P E+ TL + + A++ I EGV+A+ +G
Sbjct: 183 IIWSILFCALVGLLGTALVKVLKRILFGLPEYESTLFEQRQAMLQSIKEGVIAVDDSG 242
Query: 256 TIGVHNEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNIRILY 308
+ + N AQ+++ TL P E + GR+L
Sbjct: 243 EVTLINHAAQALLDYRKTDQDARLSTLSHAWSQVVDISEVLRDGTFRRDEEIIVKGRLLL 302
Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRIMTHALRAQRHEFANRIHTATGLI 368
++ PVR + +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 VNTVPVRSNGEIIIGAISTFRDKTEVRQLMQRLDGMVNYADALRERSHEFMNKLHVILGLL 362
Query: 369 DAGRVHDAEFLGDISRGGQSHPLIGSAHLNXXXXXXXXXXXXXXXXXKGVSLRINSDT 428
++ + N + L+ + + G SL I+SD+
Sbjct: 363 HLKSYKQLEAYIIKTANNYQEEIGLL-LGKIKSPIIAGFLLSKITRASDFGHSIVISSDS 421
Query: 429 LILGTVKDPEDVATI---LGNLINNAIDAAVAGEAPRWIBLTLMDDADTLVISVADSGP 484
+ + ED T+ LGNLI NA++ A++ E+ I ++L L V+D GP
Sbjct: 422 QLPDN--NNEDQVTVLITALGNLIENALE-ALSQESGGEISVSLHYRHGWLHCEVSDDGP 478
Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARLSEHGDDVWVIDRGTEGAV- 541
GI PE ++ +F S+ ER G+GL L + + GG VI +E G
Sbjct: 479 GIEPERIEAIFKEGVS---SKGAER---GVGLALVKQVEALGG---VISVESEPGIFT 529
Query: 542 -FGVKLP 547
F V+LP
Sbjct: 529 QFFVQLP 535

>gi|16128602|ref|NP_415152.1| putative sensor-type protein [Escherichia coli K12]
 gi|2500761|sp|P77510|DPIB_ECOLI Sensor kinase dpiB (Sensor kinase cita)
 gi|7428878|pir|A64796 signal-transducing histidine kinase homolog b0619 - Escher
 coli (strain K-12)
 gi|1778536|gb|AAB40819.1| sensor kinase Cita homolog [Escherichia coli]
 gi|1786837|gb|AAC73720.1| putative sensor-type protein [Escherichia coli K12]
 gi|4062236|dbj|BAA35255.1| Sensor kinase Cita [Escherichia coli K12]
 gi|4062242|dbj|BAA35261.1| Sensor kinase Cita [Escherichia coli K12]
 Length = 552

Score = 153 bits (387), Expect = 7e-36

Identities = 145/559 (25%), Positives = 245/559 (43%), Gaps = 44/559 (7%)

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMTEAHTALSIGRSVASN 68
 K F + F RI ++ + V+A F D + A++ + +ASN
 Sbjct: 8 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYLTlhVRDMAMNQAKIIASN 67

Query: 69 PQIREEVALDTQTGANPSAEELADGDIQAVAOAANE---RTGALFVVITDGLGIRLSHPD 125
 + V D + +A AN+ T +VVI D IRL HP+
 Sbjct: 68 DSVISAVKTR-----DYKRLATIANKLQRDITDFDYVVIGDRHSIRLYHPN 112

Query: 126 EERLGEQVSTSFEEAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDS 184
 E++G + + + A+ +GE G++G + RAK PIF D V +G VS+G+
 Sbjct: 113 PEKIGYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTFIFDDDGKV-IGVVSIGYLVSK 171

Query: 185 VYSRLPMFLAALA--LISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVID 242
 + S FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+
 Sbjct: 172 IDSWRAEFLLPAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQEQEALFS 229

Query: 243 GIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXHGOHPE 298
 + EG++A+ P+G I N A+ M+G G+ + E + +
 Sbjct: 230 SVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIVEVVRPADFFTEQIDEKRQD 289

Query: 299 TVAH-NGRILYLDHFHVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEF 357
 VA+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE
 Sbjct: 290 VVANFNGLSVIANREAIRSGDDLLGAIISFRSKDEISTLNAQLTQIKQYVESLRTLREH 349

Query: 358 ANRIHTATGLIDAGRVDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXX 415
 N + T GL+ ++ + L + LI S +
 Sbjct: 350 LNWMSTLNGLL---QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRVAGLLFGKVQRA 406

Query: 416 XEKGVSRLRI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDA 472
 E G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+
 Sbjct: 407 RELGLKMIIVPGSQLSQLPPLDSTEFAAIVGNLLDNAFEASLRSDGKNKIVELFLSDEG 466

Query: 473 DTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVW 530
 D +VI VAD G G+PE + +F E E HGIGL L + GG V
 Sbjct: 467 DDVVIEVADQCCGVPESLRDKIFEQGVSTRADEPGE---HGIGLYLIASVYVTRCGG-VI 521

Query: 531 VIDRGTEGAVFGVKLPV 549
 ++ G +F + +P V
 Sbjct: 522 TLEDNPPCGTLFSIYIPKV 540

>gi|16762986|ref|NP_458603.1| two-component sensor kinase [Salmonella enterica sub
 serovar Typhi]

gi|29144473|ref|NP_807815.1| two-component sensor kinase [Salmonella enterica sub
serovar Typhi Ty2]
gi|25298489|pir|AH1023 two-component sensor kinase (EC 2.7.3.-) [imported] - Sal
enterica subsp. enterica serovar Typhi (strain CT18)
gi|16505293|emb|CAD09289.1| two-component sensor kinase [Salmonella enterica subs
serovar Typhi]
gi|29140111|gb|AAO71675.1| two-component sensor kinase [Salmonella enterica subsp
serovar Typhi Ty2]
Length = 543

Score = 153 bits (387), Expect = 7e-36
Identities = 143/547 (26%), Positives = 254/547 (46%), Gaps = 42/547 (7%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++ T ++++ A + V+ + I+ + + AL++ RS+A +P IRE +
Sbjct: 15 MKLGTTVILMVSAVLFSVLVVVHLIYFSQISSMTRDALADKALAVARSLADSPAIREGLK 74

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
P AE IQ +++A ++ G LF+V+T+ GIR SHP+ +R+G+
Sbjct: 75 -----KPPAES-----GIQPLSEAVSQHNGFLFIVVTNMQGIRYSHPETQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVFIAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A++G+E +A G L + R P++ + +G V++G E V ++ +
Sbjct: 124 DILLALOGKENVAINRGFLAKALRVFTFVY-DEHHRQIGVVAIGLELSHVTQQINNSRGS 182

Query: 196 LALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G L+G+ + + +R+ GL+P E+ TL + + A++ I EGV+A+ +G
Sbjct: 183 IIWSILFGALVGLLGTALVKVLKRILFGLPEYEISTLFPEQRQAMLSIQEKGVIADGSG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG---RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNGRILY 308
+ + N AQ+++ TL P E + GR+L
Sbjct: 243 EVTLINHAAQALLDYRKTDQDARLSTLSHAWPQVVDISEVLRDGTFRRDEEIIVKGRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
++ FVR + +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 VNTVPVRSNGEIIIGAISTFRDKTEVRQLMQRLDGMVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRGGQSHPLIGSAHLNEXXXXXXXXXXXXXXKEGVSLRINSOT 428
++ + N + L+ + + G SL I+SD+
Sbjct: 363 HLKSYKQLEAYIIKTANNYQEEIGLL-LGKIKSPIIAGFLLSKITRASDFGHSLSVSSDS 421

Query: 429 LILGTVKDPEDVATI---LGNLINNAIDAAGEAPRWIELTLMDDADTLVISVADSGP 484
+ + ED T+ LGNLI NA++ A++ E+ I ++L L V+D GP
Sbjct: 422 QLPDN--NNEDQVTVLITALGNLIENALE-ALSQESGGEISVSLHYRHGWLHCEVSDDGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEGAV- 541
GI PE ++ +F S+ ER G+GL L + + GG VI +E G
Sbjct: 479 GIEPERIEAIFKGVGS---SKGAER---GVGLALVKQVEALGG---VISVESEPGIFT 528

Query: 542 -FGVKLP 547
F V+LP
Sbjct: 529 QFFVQLP 535

>gi|26246600|ref|NP_752639.1| Sensor kinase dpiB [Escherichia coli CFT073]
gi|26106999|gb|AAN79183.1| Sensor kinase dpiB [Escherichia coli CFT073]
Length = 572

Score = 153 bits (386), Expect = 9e-36

Identities = 145/556 (26%), Positives = 242/556 (43%), Gaps = 38/556 (6%)

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMDQMKTAEHTALSIGRSVASN 68
K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 28 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYLTLLHVRDMAMNQAKIIASN 87

Query: 69 PQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEER 128
I V + LA +A T +VVI D IRL HP+ E+
Sbjct: 88 DSIIISAVK-----TRDYKRLA-----TIADKLQRDTDFDYVVGDRHSIRLYHPNPEK 135

Query: 129 LGEQVSTSFEAAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYS 187
+G + + A+ +GE G++G + RAK PIF D V +G VS+G+ + S
Sbjct: 136 IGYPMQFTKPGALEKGESYFITGKGSIGMAMRAKTPIFDDDGKV-IGVVSIGYLVSKIDS 194

Query: 188 RLPMFLAALA--LISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGID 245
FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+ +
Sbjct: 195 WRAEFLLPAGVFVLLGILMLLSWFLAAHIR--RQMMGMEPKQIARVVRQOEALFSSVY 252

Query: 246 EGVLAISPNGTIGVHNEQAQSMIGAGPMS---GRTLKEXXXXXXXXXXXHGXHPETVA 301
EG++A+ P+G I N A+ M+G G+ + E + + VA
Sbjct: 253 EGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIAEVVRPADFFTEQIDEKRQDVVA 312

Query: 302 H-NGRILYLDHFHVRGDDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANR 360
+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE N
Sbjct: 313 NFNGLSVIANREAIRSGDDLGAIIISFRSKDEISTLNAQLTQIKQYVBSLRTL RHEHLNW 372

Query: 361 IHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXXXXEK 418
+ T GL+ ++ + L + LI S + E
Sbjct: 373 MSTLNGLL---QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRQVAGLLFGKVQRAREL 429

Query: 419 GVSLRI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-ACEAPRWIELTLMDDADTL 475
G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+ D +
Sbjct: 430 GLKMVIVPGSQLSQLPPGLDSTEFAAIVGNLLDNAFEASLRSDGNKSVELFSLDEGDDV 489

Query: 476 VISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVID 533
VI VAD G G+PE + +F E E HGIGL L + GG V ++
Sbjct: 490 VIEVADQCGVPESLRDKIFEQGVSTRADEPGE---HGIGLYLIASYVTRCGG-VITLE 544

Query: 534 RGTEDGAVFGVKLPGV 549
G +F + +P V
Sbjct: 545 DNDFCGTLFSIYIPKV 560

>gi|15804717|ref|NP_290758.1| putative 2-component sensor protein [Escherichia coli EDL933]
gi|15834361|ref|NP_313134.1| DcuS; two-component sensor protein [Escherichia coli]
gi|16131951|ref|NP_418549.1| putative 2-component sensor protein [Escherichia coli]
gi|2506733|sp|P39272|DCUS_ECOLI Sensor protein dcuS
gi|7428874|pir|D65222 hypothetical 60.6 kD protein in dcuB-lysU intergenic region Escherichia coli (strain K-12)
gi|25298481|pir|C91267 two-component sensor protein DcuS ECs5107 [imported] - Es coli (strain O157:H7, substrain RIMD 0509952)
gi|25298486|pir|H86107 probable 2-component sensor protein yjdh [imported] - Es coli (strain O157:H7, substrain EDL933)
gi|1790567|gb|AAC77086.1| putative 2-component sensor protein [Escherichia coli K]
gi|12519101|gb|AAG59324.1| putative 2-component sensor protein [Escherichia coli EDL933]
gi|13364584|dbj|BAB38530.1| two-component sensor protein DcuS [Escherichia coli O length = 543

Score = 152 bits (384), Expect = 2e-35

Identities = 133/529 (25%), Positives = 242/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMQMKTEAHTALSIGRSVASNPQIREEVA 76
++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVSAVLFSVLLVHLYFSQISDMTRDGLANKALAVARTLADSPEIRQGLQ 74

Query: 77 LDTQTGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPAQRIGQPFKGD 123

Query: 136 SFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILKALNGEENVAINRGFLAQAALRVFTPIY-DENHKQIGVVAIGLELSRVTTQQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G+L+G+ + + +++ GL+P E+ TL + + A++ I EGV+A+ G
Sbjct: 183 IIWSVLFGMLVGLIGTCILVKVLKILFGLFYEISTLFEQRQAMLSIKEGVVAVD DRG 242

Query: 256 TIGVENEQAQSMIGAGPMSG---RTLKEXXXXXXXXXXXXXXHCQHP---ETVAHNIRILY 308
+ + N+ AQ ++ TL P E + R+L
Sbjct: 243 EVTLINDAAQELLNRYKRSQDDEKLSTLSHSWSQVVDVSEVLRDGTFRRDEBITIKDRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368
++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 INTVPVRSNGVIIGAISTFRDKTEVRKLMQRDLGLVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKGVSLRINS 426
+++ + N + IGS + + G +L +NS
Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLLGKIKSPVIAGFLISKINRATDLGHTLIINS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINAIDAAVAGEAPRWIELTLMDDADTLVISVADSGP 484
++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP
Sbjct: 420 ESQLPDSGSEDQVATLITTLGNLIENALE-ALGPEPGGBISVTLHYRHGWLHCEVND DGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARSHGCDVWV 531
GI P+ +D +F SE G+GL L + + GG + V
Sbjct: 479 GIAPDKIDHIFDKGVSTKGSE-----RGVGLALVKQQVENLGGSIAV 520

>gi|536970|gb|AAA97025.1| ORF_f543 [Escherichia coli]
Length = 543

Score = 152 bits (384), Expect = 2e-35

Identities = 133/529 (25%), Positives = 242/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMQMKTEAHTALSIGRSVASNPQIREEVA 76
++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVSAVLFSVLLVHLYFSQISDMTRDGLANKALAVARTLADSPEIRQGLQ 74

Query: 77 LDTQTGANPSABELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPAQRIGQPFKGD 123

Query: 136 SFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILKALNGEENVAINRGFLAQAALRVFTPIY-DENHKQIGVVAIGLELSRVTTQQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G+L+G+ + + +++ GL+P E+ TL + + A++ I EGV+A+ G
Sbjct: 183 IIWSVLFGMLVGLIGTCILVKVLKILFGLPEYESTLFEQRQAMLQSIKEGVVAVDDRG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHGQHP--ETVAHNGRILY 308
+ + N+ AQ ++ TL P E + R+L
Sbjct: 243 EVTLINDAAQELLNYRKSQDDEKLSTLSHWSQVVDVSEVLRDGTFRDEEITIKDRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRDIEELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368
++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 INTVPVRSNGVIIGAISTFRDKTEVRKLMQRLDGLVNYXDALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXKGVSLRINS 426
+++ + N + IGS + + G +L +NS
Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLLGKIKSPVIAGFLISKINRATDLGHTLILNS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTMDADTLVISVADSGP 484
++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP
Sbjct: 420 ESQLPDSGSEDQVATLITTLGNLIENALE-ALGPEPGGEISVTLHYRHGWLHCEVNDDGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERETHGHGIGLKLCLARSHGGDVWV 531
GI P+ +D +F SE G+GL L + + GG + V
Sbjct: 479 GIAPDKIDHIFDKGVSTKGS-----RGVGLALVKQQVENLGGSIIV 520

>gi|24115306|ref|NP_709816.1| putative 2-component sensor protein [Shigella flexne
gi|30064694|ref|NP_838865.1| putative 2-component sensor protein [Shigella flexne
2457T]
gi|28558086|sp|P59341|DCUS SHIFL Sensor protein dcus
gi|24054605|gb|AA045523.1| putative 2-component sensor protein [Shigella flexneri
gi|30042954|gb|AAP18676.1| putative 2-component sensor protein [Shigella flexneri
2457T]
Length = 543

Score = 152 bits (383), Expect = 2e-35
Identities = 133/529 (25%), Positives = 242/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMDQMKTAEHTALSIGRSVASNPQIREEVA 76
++ +T +++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVSVAFLSVLLVHLYFSQISDMTRDGLANKALAVARTLADSPEIRQGLQ 74

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPEAQRIGQPFKGD 123

Query: 136 SFEEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILNALNGEENVAINRGFLAQAALRVFTPIY-DENHKQIGVVAIGLELSRVTTQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G+L+G+ + + +++ GL+P E+ TL + + A++ I EGV+A+ G
Sbjct: 183 IIWSVLFGMLVGLIGTCILVKVLKILFGLPEYESTLFEQRQAMLQSIKEGVVAVDDRG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG----RTLKEXXXXXXXXXXXXXXHGQHP--ETVAHNGRILY 308
+ + N+ AQ ++ TL P E + R+L
Sbjct: 243 EVTLINDAAQELLNYRKSQDDEKLSTLSHWSQVVDVSEVLRDGTFRDEEITIKDRLLL 302

Query: 309 LDFHPVRRGDQDLGYVVTIRDRDIEELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368
++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+

Sbjct: 303 INTVPVRSNGVIIGAISTFRDKTEVRKLMQRLDGLVNYADALRERSHEPMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKGVSLRINS 426

+++ + N + IGS + + G +L +NS

Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLGKIKSPVIAGFLISKINRATDLGHTLILNS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLVISVADSGP 484

++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP

Sbjct: 420 ESQLPDSGSEDQVATLITLGNLIENALE-ALGPEPGGEISVTLHYRHGWLHCEVNDDGP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVVW 531

GI P+ +D +F SE G+GL L + + GG + V

Sbjct: 479 GIAPDKIDHIFDKGVSTKGSE-----RGVGLALVKQVENLGGSIIV 520

>gi|27365978|ref|NP_761506.1| Signal transduction histidine kinase regulating citr
metabolism [Vibrio vulnificus CMCP6]

gi|27362178|gb|AA011033.1| Signal transduction histidine kinase regulating citrat
metabolism [Vibrio vulnificus CMCP6]

Length = 539

Score = 151 bits (381), Expect = 4e-35

Identities = 146/533 (27%), Positives = 238/533 (44%), Gaps = 41/533 (7%)

Query: 17 IRPATRILVIQVAT--VALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREE 74

I F R+LVI + + L++ + G F A L Q + E AL + R +A++ + E

Sbjct: 6 ISPRKRMLVIMTSLGLIELLILVAAG-FAYLKYSQ-BQEMGQKALGVARFLATSTTVIEL 63

Query: 75 VALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV- 133

+ E D Q + + GA F+V+ D GIRL HP +ERLG +

Sbjct: 64 I-----ENRDDVTYQOKFRELTQALGAFFIVGDRGIRLIHPVDERLGLPMR 111

Query: 134 -STSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVFPVGEVSVGFERDSVYSRLPMF 192

+ A GE ++ G+LG S R K +F V +G VSVG+ D + R+ F

Sbjct: 112 GGDNARALEEGEAYISTARGLSVRGKAAVFNSSAGEV-IGVVSVGYLLDRLQDRIEFP 170

Query: 193 LAALALISVLGILIGVGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252

L +++L + V+ R+++R LG +PEE+ L + I EGVL++

Sbjct: 171 AWFLIAMTLLVVAANALVSNYASRKFRAILGFEPPEIGRLYGELDVMTSTIKEGVLSID 230

Query: 253 PNGTIGVHNEQAQSMIGAGPMS--GRTLKEXXXXXXXXXXXXXXHQ--HPETVAHNGRILY 308

+G + N A ++G P + L + GQ H + N + L

Sbjct: 231 SSGVLRISNRSAAQILGLDPAQVLNKPFLSDALPASDLVRVLETGQEDHDIELYLNQKRLI 290

Query: 309 LDFHPVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTALRAQRHEFANRIHTATGLI 368

+ PV + +G V + R R +I EL+E+L + LR+Q HE N+++T +GL+

Sbjct: 291 ANRSPVYVEGKIVGAVSSFRRLRDEISELTEQLSQTKEYADLLRSQTHEHRNKLTISGLV 350

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXXXKGVSLRINS 426

G + + +G + LI + + E G+ L +

Sbjct: 351 QMGELDAVQQLIG---QETAHYQGLIEFLRDTIKDPLVAGMLLGKTERARELGLELVVEE 407

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA---AVAGE-----APRWIELTLMDDADTLV 476

+ L +PED+ TILGNLI+NA DA A+A E + R IE+++ D ++

Sbjct: 408 GARLEPLSAWLNPNEDITITLGNLIDNAFDATMSAIAQEGNFARSRTIEVSISPYGTEVI 467

Query: 477 ISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDV 529

+ V D G G+P+ F+T + ++ T G+GL L LA + G +

Sbjct: 468 LEVQDQGCGLPKQ---FSTEQLLEKGISSKATSTRGVGLYLVNQLAARYCGSI 517

>gi|26250939|ref|NP_756979.1| Sensor protein dcuS [Escherichia coli CFT073]
gi|28558085|sp|P59340|DCUS_ECOL6 Sensor protein dcuS
gi|26111371|gb|AAN83553.1| Sensor protein dcuS [Escherichia coli CFT073]
Length = 543

Score = 151 bits (381), Expect = 4e-35

Identities = 133/529 (25%), Positives = 241/529 (45%), Gaps = 37/529 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
++ +T ++++ A + V+ + I+ + D + + AL++ R++A +P+IR+ +
Sbjct: 15 MKLSTTVILMVSAVLFSVLLVHLLIYFSQISDMTRDGLANKALAVARTLADSPETRQGLQ 74

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS-T 135
Q + IQA+A+A +R LF+V+TD +R SHP+ +R+G+
Sbjct: 75 KKPQ-----ESGIQAIAEAVRKRNDLLFIVVTDMSLRYSHPEAQRIGQPFGKD 123

Query: 136 SFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ GEE +A G L + R PI+ ++ +G V++G E V ++ +
Sbjct: 124 DILKALNGEENVAINRGFLAQALRVFTPIY-DENHKQIGVVAIGLELSRVTTQINDSRWS 182

Query: 196 LALISVLGILIGVGVAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ + G+L+G+ + +++ GL+P E+ TL + + A++ I EGV+A+ G
Sbjct: 183 IIWSVLFGMLVGLIGTCILNVNLLKILFGLPEYEISTLFEQRQAMLQSIKEGVVAVDDRG 242

Query: 256 TIGVHNEQAQSMIGAGPMSG---RTLKEXXXXXXXXXXXXXXHGQHP---ETVAHNGRILY 309
+ + N+ AQ ++ TL P E + R+L
Sbjct: 243 EVTLINDAAQELLNRYKRSQDDEKLSTLSHWSQVVDVSEVLRDGTPTRRDEEITIKORLLL 302

Query: 309 LDFHFPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
++ PVR +G + T RD+T++ +L +RLD + ALR + HEF N++H GL+
Sbjct: 303 INTVPVRSNGVTIIGAISTFRDKTEVRKLMQRLDGLVNYADALRERSHEFMNKLHVILGLL 362

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINS 426
+++ + N + IGS + + G +L +NS
Sbjct: 363 HLKSYKQLEDYILKTANNYQEE---IGSLGKIKSPVIAGFLISKINRATDLGHTLILNS 419

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGP 484
++ + G+ + T LGNLI NA++ A+ E I +TL L V D GP
Sbjct: 420 ESQLPDSGSEDQVATLITLGNLIENALE-ALGPEPGGEISVTLHYRHGWLHCEVNDGDP 478

Query: 485 GI-PEGVD-VFATATQIGDSEDNERTHGHGIGLKLCLARASHGGDVWV 531
GI P+ +D +F SE G+GL L + + GG + V
Sbjct: 479 GIAPDKIDHIFDKGVSTKGSE-----RGVGLALVKQQVENLGGSIAV 520

>gi|37679787|ref|NP_934396.1| putative sensor kinase Cita [Vibrio vulnificus YJ016]
gi|37198532|dbj|BAC94367.1| putative sensor kinase Cita [Vibrio vulnificus YJ016]
Length = 539

Score = 150 bits (380), Expect = 5e-35

Identities = 147/533 (27%), Positives = 239/533 (44%), Gaps = 41/533 (7%)

Query: 17 IRFATRILVIQVAT--VALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREE 74
I F R+LVI + + L++ + G FA L Q + E AL + R +A++ + E
Sbjct: 6 ISFRKRMLVIMTLISGLIELLILVAAG-FAYLKYSQ-EQEMGQKALGVARFLATSTTVIEL 63

Query: 75 VALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV- 133
+ EL QA++ A F+V+ D GIRL HP +ERLG +
Sbjct: 64 IENRDNVTYQQKFRELT----QALSAA-----FIVVGDREGIRLIHPVDERLGLPMR 111

Query: 134 -STSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMF 192
+ A GE ++ G+LG S R K +F V +G VSVG+ D + R+ F
Sbjct: 112 GGDNARALEEGEAYISTARGLGYSVRGKA AVFNSAGEV-IGVVS VGYLLDRLQDRIEPF 170

Query: 193 LAALALISVLGILIGVGVAMGMRWRERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALS 252
L +++L + V+ R+++R LG +PEE+ L + I EGVL++
Sbjct: 171 AWFLITMTLLVVAANALVSNYASRKPFQRAILGFEEIGRLYGELDVTMSTIKEGVLSID 230

Query: 253 PNGTIGVHNEQAQSMIGAGPMS--GRTLKEXXXXXXXXXXXXXXHGQ--HPETVAHNGRILY 308
+G + N A ++G P + L + GQ H + N + L
Sbjct: 231 SSGVLR SINRSAAQILGLDPAQVLNKP LSLDALPASDLYRVLETGQEDHDIELYLNQKRLI 290

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
+ PV + +G V + R R +I EL+E+L + LR+Q HE N+++T +GL+
Sbjct: 291 ANRSPVYVEGKIVGAVSSPRLRDEISELTEQLSQTKEYADLLRSQTHEHRNKINTISGLV 350

Query: 369 DAGRVHDAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXXXXXXEGVSLRINS 426
G + + +G + LI + + E G+ L +
Sbjct: 351 QMGELDAVQQLIG---QETAHYQGLIEFLRDTIKDPLVAGMLLGKTERARELGLELVVEE 407

Query: 427 DTLI--LGTVKDPEDVATILGNLINNAIDA--AVAGE-----APRWIELTLMDDADTLV 476
+ L +PED+ TILGNLI+NA DA A+A E + R IE+++ D ++
Sbjct: 408 GARLEPLSAWLNPEEDITITILGNLIDNAFDATMSAIAQEGNFARSRTIEVSISDYGTEVI 467

Query: 477 ISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDV 529
+ V D G G+P+ F+T + ++ T G+GL L LA +GG +
Sbjct: 468 LEVQDQGCGLPKQ---FSTEQLLEKGISSKATSTRGVGLYLVNQLAARYGSI 517

>gi|21223794|ref|NP_629573.1| putative two-component sensor kinase [Streptomyces c
A3(2)]
gi|6941977|emb|CAB72411.1| putative two-component sensor kinase [Streptomyces coe
A3(2)]
Length = 552

Score = 149 bits (376), Expect = 1e-34
Identities = 150/543 (27%), Positives = 239/543 (44%), Gaps = 35/543 (6%)

Query: 19 FATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREVALD 78
A ++ +Q +A+VV + Q + A A ++ ++A +P + E +
Sbjct: 11 LAGQLFAMQAVLIAVVVVG YALFSYISDRGQAEZAAQRQARAVSLAIADSPSVAEAI RTP 70

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSF 138
T +Q A T FV I + GIR +HP+ +G E
Sbjct: 71 DPTAL-----LQPYAVRVMRDTDVDFVTIMNPEGIRWTHPEPTTEIGHLFOGHIE 119

Query: 139 AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALAL 198
A RG+ TGTLG S RA PI D VG VS G + + + R L AL+
Sbjct: 120 RAQRGQTFETETYTGTLGPSVRAVTPIV--DDGRIVGLVSAGIKVEEISKRAQEQLTALSG 177

Query: 199 ISVLGILIGVGVAMGMRWRERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIG 258
++ +L+G + R R T G+ +EL + A + + EG+L L +
Sbjct: 178 VAAGALLLGAVGTYVINARLRRHTHGMNADEL SRMHDYHQAALHAVREGLLM LDGQYRVA 237

Query: 259 VHNEQAQSMIGA-GPMSGRTLKEXXXXXXXXXXXXXXHGQHHPETVAHNG--RILYLD FHPVR 315

+ N+ + ++G G + G ++ + + H R+L ++ PV
Sbjct: 238 LINDGGRELLGVRGDIVGASVADLGLPSQLTGALLASEPRVDEVHLAAERVLVVNTSPVS 297
Query: 316 RGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDH 375
G++ G VVT+RD T++ L+ L+S R T ALR+Q HE ANR+HT LI+ GR +
Sbjct: 298 GGERR-GTVVTLRDVTEQLSLTGELNSERGFTQALRSQAHEAANRLHTVVSLIELGRAEE 356
Query: 376 AAEF-LGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINSDTLILGTV 434
A EF ++ + ++ A ++E E+GV L ++ D+ + +
Sbjct: 357 AVSFATAELELAQALTDQVV--AAVSEFVLAALLLGKTAQANERGVELVVVSQDSRLDDGL 414
Query: 435 KDP----EDVATILGNLINNAIDAAVAGEAPRWIELTLMDDA-----DTLVISVADSGPG 485
P D+ TILGNL++NA+DA G P + + +A LV+ V+D+G G
Sbjct: 415 LPPSLPARDLVTTILGNLVDNAVDAT-QGAVPSRVTVAAYTEASGAGGSELVLRVSDTGAG 473
Query: 486 I-PEGVDVFATATQIGDSEDNERETHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGV 544
+ P D+ Q G S G G+GL L R R HGG + V + GA F
Sbjct: 474 VDPAHADL--VFQRGYSTKPAGEGGRGLGLALVRQAVRRHCGALTVTE-AEGCGARFEA 529
Query: 545 KLP 547
+LP
Sbjct: 530 RLP 532

>gi|2734636|gb|AAC28951.1| histidine kinase [Escherichia coli]
Length = 539

Score = 148 bits (374), Expect = 2e-34
Identities = 138/527 (26%), Positives = 232/527 (44%), Gaps = 43/527 (8%)

Query: 9 KNFKEVDIIRFATRILVIQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASN 68
K F + F RI ++ + V+A F D + A++ + +ASN
Sbjct: 8 KQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTASFEDYTLHVRDMAMNQAKIIASN 67
Query: 69 PQIREEVALDTQTGANPSAEELADGDIQAVAQAANE---RTGALFVVTIDGLGIRLSHPD 125
+ V 'D + +A AN+ T +VVI D IRL HP+
Sbjct: 68 DSVISAVKTR-----DYKRLATIANKLQRTDFDYVVIGDRHSIRLYHPN 112
Query: 126 EERLGEQVSTSFEEAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDS 184
E++G + + + A+ +GE G++G + RAK PIF D V +G VS+G+
Sbjct: 113 PEKIGYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTIPIFDDDGKV-IGVVSIGYLVSK 171
Query: 185 VYSRLPMFLAALA--LISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVID 242
+ S FL +A + +LGIL+ + + R R +G++P+++ +V+ Q A+
Sbjct: 172 IDSWRAEFLLPMAGVFVLLGILMLLSWFLAAHIR--RQMMGMPEKQIARVVRQQEALFS 229
Query: 243 GIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXHGHQHE 298
+ EG++A+ P+G I N A+ M+G G+ + E + +
Sbjct: 230 SVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLKPIVEVVRPADFFTEQIDEKRQD 289
Query: 299 TVAH-NGRILYLDHFVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEF 357
VA+ NG + + +R GD LG +++ R + +I L+ +L ++ +LR RHE
Sbjct: 290 VVANFNGLSVIANREAIRSGDDLGAIIISFRSKDEISTLNAQLTQIKQYVESLRTLREH 349
Query: 358 ANRIHTATGLIDAGRVDHAAEFLGDISRNGGQSHPLIGSAH--LNEXXXXXXXXXXXXXX 415
N + T GL+ ++ + L + LI S +
Sbjct: 350 LNWMTLNGLL---QMKEYDRVLAMVQGESQAQQQLIDSLREAFADRQVAGLLFGKVQRA 406
Query: 416 XEKGVSLEI--NSDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDA 472

E G+ + I S L D + A I+GNL++NA +A++ + E + +EL L D+
Sbjct: 407 RELGLKMIIVPGSQLSQLPPLGLDSTEFAAIVGNLLDNAFEASLRSDGKIVELFLSDEG 466

Query: 473 DTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKL 517
D +VI VAD G G+PE + +F E E HGIGL L

Sbjct: 467 DDVVIEVADQGCVPESLRDKIFEQGVSTRADEPGE----HGIGLYL 509

>gi|15612960|ref|NP_241263.1| two-component sensor histidine kinase [Bacillus halo
gi|25298482|pir|E83699 two-component sensor histidine kinase BH0397 (imported) -
halodurans (strain C-125)
gi|10173010|dbj|BAB04116.1| two-component sensor histidine kinase [Bacillus halod
Length = 532

Score = 147 bits (372), Expect = 4e-34

Identities = 147/544 (27%), Positives = 255/544 (46%), Gaps = 42/544 (7%)

Query: 21 TRILVIQVATVALVVAICTGI----FAVLMMQMKTEASHTALSIGRSVASNPQIREEVA 76
T++ ++ A V LVV + I +V +++++ E A++I R+VA + +
Sbjct: 6 TKLSILITALVCLVVIVALIITDLLVSVATSERLQSNIEEKAIAISRTVA-----KAQWV 60

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTS 136
+D G EE +Q T LF+V+ D GIR SHP+ E +G++
Sbjct: 61 ID---GLENEEEWR---VQTYTMEIQSATDVLFIIVMDMEGIRKSHPNPEEIGKRFVGG 114

Query: 137 FE-AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
E AA+ G E ++ TGTLG S RA PIF D +G V+VG V L +
Sbjct: 115 DEVAALEGREHVSISTGTLGESLRAFTPIFN-DHGEQLGAVAVGISLQEVNDVLADNHTS 173

Query: 196 LALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+ SV+GI++G+ A+ + +R LGL+P E+ +++ ++A++ E ++A+ G
Sbjct: 174 ILKGSVIGIIVGIIGALIVASYIKRALLGLEPFEIAKILEERSAMLQSAREAIIVDSKG 233

Query: 256 TIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXX-----HGQHPETVAHNGRILYL 309
TI + N+ A ++ MSG + + + E NG + +
Sbjct: 234 TITLVNKSALNLFKAGMSGDPGKVKVTEFMPSTRLEWVLKTRQPEFDEEQQMNGMTILV 293

Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ P+ D+ +G + T RD T+I + +++L V+ ALRAQ HEF N++H G++
Sbjct: 294 NRVPIIVNDEVVGAISTFRDLTEIKQQAQQLTGKLYVEALRAQSHEFMNKLHVILGMVK 353

Query: 370 AGRVHDAAEFLGDI--SRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINS 427
+ +++ I R+ +H + + + EK ++L + +
Sbjct: 354 TESIYDELNDYIHQIVNHRSTELNHVI---KRIKDSVLGAFILGKLSYAREKHITLDVQTK 410

Query: 428 TLILGTVKDP--EDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPG 485
++I + ++ TILGNLI+NA++A + + + + L + L I V D+GPG
Sbjct: 411 SVIPKASSEQMVHELITILGNLIDNALEAVIKAKE-KTVLVQLEYSNERLHIRVQDTGPG 469

Query: 486 IPEGV--DVFATATQIGDSEDNERTHGHGIGLKLALARSHGGDVVIDRGTEDGAVFG 543
IP+G D+F + G S E G GL L + GG + R T G F
Sbjct: 470 IPDGEQGDIF----KKGYSTKGE---NRGYGLYLKQSVKLGGAMEYESRAT--GMTFY 520

Query: 544 VKLP 547
V +P

Sbjct: 521 VDIP 524

>gi|30018746|ref|NP_830377.1| Two component system histidine kinase [Bacillus cere
gi|29894287|gb|AAP07578.1| Two component system histidine kinase [Bacillus cereus
Length = 535

Score = 147 bits (370), Expect = 7e-34
Identities = 130/527 (24%), Positives = 245/527 (46%), Gaps = 48/527 (9%)

Query: 41 IFAVLMMQMKTEAEHTALSIGRSVASNPQIREEEVALDTQTGANPSABELADGDIQAVAQ 100
+F ++ + + + AL + ++VA+ P+I+E + NP++ IQ +A+
Sbjct: 32 LPYYILSETVEEQIGKRALHVAKTVAAIPEIQEAFQKE-----NPAS-----IIQPIAE 80

Query: 101 AANERTGALFVVITDGLGIRLSHPDEERLGEQV--STSFZAAAMRGEETMAWETGTLGASA 158
T A F+V+ + GIR +HP+ +++GE++ + + G+ ++ TG+LG S
Sbjct: 81 KIRMDTEADFIVGNKEGIRYAHPERDKIGEXMVGGDNKGVLLGKSYVSKATGSLGPSL 140

Query: 159 RAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRW 218
R KVPI ++ + +G VSVGF ++ + ++ + I+++G+LIGV ++ +
Sbjct: 141 RGKVPINQENEI-IGVSVVGFSMADIHGAVEVYCKRVFWITIIGLLIGVIGSIYLAAS 199

Query: 219 ERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMS---G 275
+R+ G++PER+ +L + + VI + EG++ + NG I + N+ A ++ G
Sbjct: 200 KRMMFGMEPEEISSLYEEHSTVIQSVREGIIVIDKNGMISLVNQAAYDILSLDKQQNIIG 259

Query: 276 RTLKEXXXXXXXXXXXXXXHG--QHPETVAHNGRILYLDHFPVRRGDQDLGYVVTIRDRDI 333
+ G Q + G+ + + P++ ++ G V ++R ++++
Sbjct: 260 EFILNVIPNSTILDVLQTGEEQFDRQLNIKGQAVIANRLPIKVKNKVTGVVSSLRLKSEM 319

Query: 334 IELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFLGD---ISRNGGQ- 389
+L+ L + T ALRAQ HE+ N ++T +GLI DA E + + ++ Q
Sbjct: 320 DQLTAELSQTQYTEALRAQAHEYNLLYTLGSLIQLESYEDALELIHKETAVYQDFVQF 379

Query: 390 -----SHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEG---VSLRINSDTLILGTVKDPEDVA 441
+P +G + E G +S I S+ V
Sbjct: 380 IMKRIQNPWLGGILIGFYNRARELKIDFMLDRESGLEKLSPHIESNY-----VV 428

Query: 442 TILGNLNNDAIDAAVAGEA-PRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIG 500
+ILGNLI NA +A E + + + + D + ++I V DSG GI + +
Sbjct: 429 SILGNLITNAFEAIEKNEENDKKVRMFVTDIGEEILIEVEDSGQGIHDEIITSIFYKGFS 488

Query: 501 DSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547
E ER G GL + L G + I++G GA+F + LP
Sbjct: 489 TKEGGER----GYGLAKVKELVEDLNGSI-AIEKGLGALFIIALP 530

>gi|16764002|ref|NP_459617.1| sensory histidine kinase [Salmonella typhimurium LT2
gi|16419137|gb|AA119576.1| sensory histidine kinase in two-component regulatory s
DpiA [Salmonella typhimurium LT2]
Length = 553

Score = 145 bits (367), Expect = 2e-33
Identities = 145/547 (26%), Positives = 242/547 (44%), Gaps = 36/547 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMQMKTEAEHTALSIGRSVASNPQIREEEVA 76
+ F RI ++ + +VA + D + + A++ + +ASN I V
Sbjct: 16 LAFFLRIFLLILVVSFIVAALAAQYLSASFEDYLASHVRDMAMNQAKIIASNDSTIAAVK 75

Query: 77 LDTQTGANPSABELADGDIQAVAAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTS 136
N + LA +A T +VVI D IRL HP+ E++G + +
Sbjct: 76 -----NRDYKRLA-----IANKLQRTDFDYVVGDRHSIRLYHPNPEKIGYPMQFT 123

Query: 137 FEAAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ RGE G++G + RAK PIP + +V +G VS+G+ + S FL
Sbjct: 124 KPGALERGESYFITGKGSIGMAMRAKTPIFDNEGVN-IGVVSIGYLVSKIDSWRLDFLLP 182

Query: 196 LALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+A + VL +++ + ++ R LG++P+++ +V+ Q A+ + EG++A+ P G
Sbjct: 183 MAGVFLVLLVLMMLLSWFFAAHRRQMLGMEPKQIARVVRQOEALFSSVYEGLIAVDPEG 242

Query: 256 TIGVHNEQAQSMIGAGPMSGRT-----LKEXXXXXXXXXXXXXXGHPETVAH-NGRILYL 309
I N A+ M+G P GR + E + + +A+ NG +
Sbjct: 243 HITAINRNARKMLGL-PSPGRQWLGLIAEVVNPADFFTCQIAERRQDVMANFNGLSVIA 301

Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ +R G++ LG +++ R + +I L+ +L ++ +LR RHE N + T GL+
Sbjct: 302 NREAIRSGEELLGAIISFRSKDEIATLNAQLTQIKQYVESLRTLREHLNWMSTLNGLLQ 361

Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXGKGVSLRI--N 425
E + S+ Q LI S + E G+ + I
Sbjct: 362 MKEYDRVREMVOGESQAQQQ---LIDSLRGAFADRQVAGLLFGKVQRARELGLKMVIVPG 418

Query: 426 SDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDADTLVISVADSGP 484
S L D + A I+GNL++NA +A++ E + IEL L D+ D +VI VAD G
Sbjct: 419 SQLHQLPEGLDSTEFAAIVGNLLDNAFEASLRTOEGDKTIELPLSDEGDEVVIEVADQGC 478

Query: 485 GIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVF 542
G+PE + +F E E HGIGL L + GG V ++ G +F
Sbjct: 479 GVPEALREKIFEQGVSTRTEDEPGE---HGIGLYLIASVVGRCGG-VITLEDNDPCGTLF 533

Query: 543 GVKLPKV 549
+ LP V
Sbjct: 534 SLFLPKV 540

>gi|21219651|ref|NP_625430.1| putative two component system histidine kinase [Stre
coelicolor A3(2)]
gi|10803161|emb|CAC13089.1| putative two component system histidine kinase [Strep
coelicolor A3(2)]
Length = 548

Score = 145 bits (366), Expect = 2e-33
Identities = 157/511 (30%), Positives = 252/511 (49%), Gaps = 42/511 (8%)

Query: 63 RSVASNPQIREEVALDTQTGANP--SAEELADGDIQAVAQAANE---RTGALFVVITDGL 117
R+ + + R AL Q A P ++ L +A+A N ++G V + D
Sbjct: 38 RATFNVRVEGRRTALAEQLAATPLVRSQLLRPVPQEBALAPLVNSTQTQSGVTSVTVADAH 97

Query: 118 GIRLSHPDEERLGEQVSTSFEAAMRGEETMAWETGTL----GASARAKVPIFAPDSSV-- 171
G +S D +G ++ + RG + +G L G A+V+P+
Sbjct: 98 GRIVSSTDPTLIGARLPRA-----RGAGVTSGWSGPLTVQGGRELVAQVPVLGATRQTLG 152

Query: 172 -PVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG--MRRRWERTLGLQPE 228
+G V VG +V+ RL A+ L++ LG+ G+GVA + RR +R TLGL+P
Sbjct: 153 RHLGTVMVGEADPTVWQRLSG--ASSYLLAYLGVASGLGVAGSWLLARRVKRQTLGLEPR 210

Query: 229 ELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIG-AGPMSGRTLK----EXXX 283
E+ L +++ A++ GI EGV+AL P + + NE + ++ G++L +
Sbjct: 211 EIAGLABHREAMLYGIAEGVVALDPQHRLTLVNEMGRRLDLFADCVGQSLDGLGIDGRL 270

Query: 284 XXXXXXXXXXXXHGQHP--ETVAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDIIELSERLD 341
P E V +GR+L ++ V + + LG V T+RDRT++ L +
Sbjct: 271 RDVLAGAAREAAEPRDEVVVRHGRVLVMNRMVTTKDGRPLGSVTTLRDRTELARLEREIG 330

Query: 342 SVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNE 401
S R+ + LRAQ HEFAN++HT +GLI G + ++ +++ QS + S + +
Sbjct: 331 SFRSTSELLRAQAHEFANQLHTISGLIQIGEQBEVVRYVRGLNQR-RQSLDVTLSRRVRD 389

Query: 402 XXXXXXXXXXXXXXXXKEKGVSLRINSDTLILGTVK--DPEDVATILGNLINNAIDAABA-G 458
E+ V+LR+ SD L ++ D DVAT++GNL++NA+DAA A G
Sbjct: 390 TAVAALITAKSSSLAERRVALRV-SDRTALDRLEPADAADVATVVGNLVDNAVDAAAALG 448

Query: 459 EAPR-WIELTLMDDADTLVISVADSGPGI-PE-GVDVFATATQIGDSEDNERTHGHGIGL 515
+AP W+E+ L DA ++ I V DSGPG+ PE +VF+ + ER GIGL
Sbjct: 449 DAPEAWVEVELRQDAASVEIVVRDSDSGPGVAPELAREVFSHGFTTKAARQGER----GIGL 504

Query: 516 KLCRALARSHGGDVWVIDRGTEGDAVFGVKL 546
L R + HGG++ V + T +GAVF ++
Sbjct: 505 ALTRLVCERHGGGEISVTN--TPEGAVFTARM 533

>gi|23100706|ref|NP_694173.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
gi|22778940|dbj|BAC15207.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
Length = 528

Score = 144 bits (363), Expect = 5e-33
Identities = 141/543 (25%), Positives = 247/543 (45%), Gaps = 46/543 (8%)

Query: 22 RILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVALDTQT 81
+ LV+ V ++ + ++ DQ + AL+ +V+ P+++ +
Sbjct: 8 KFLVLGCILVTAIMLMVMVLYISYERDQTRQLIGQQALTIAVSEIPEVQHVI----- 61

Query: 82 GANPSAEELADGDI-QAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--STSFE 138
E D D+ Q + +++ A F+VI D +R +HPD +++G Q+ + +
Sbjct: 62 -----EHQKDADVLQPFIERIRKQSNAEFIVIGDRNSLRYTHPD PDKVGMQMVGGDNEQ 115

Query: 139 AAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGF---RDSVYSR-LPMFLA 194
A + GE ++ G+LGAS R K PIF D + +G VSVG+ DS++ + L FL
Sbjct: 116 ALVDGENYVSIANGSLGASVRGKSPIFNSDGD I-IGIVSVGYMISYVDSLFGKQGLIGFLV 174

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
L+LI ++G+ +A +R+ T GL+P ++ + + + A+++ I EG++A
Sbjct: 175 WLSLIFIIGVAGSFLAKSIRKD---TFGLEPYQIARIYKERGALESIKEGLIATDQR 230

Query: 255 GTIGVHNEQAQSMIG-----AGPMSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYL 309
G I + N A+ M+ G L G T+ N +L +
Sbjct: 231 GHITLVNYSKEMLHIRHDVIGKFPVQEVLPNTLAYVLTEHREGSFETTI--NQTVLLV 288

Query: 310 DFHFPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ + G V + + R+D+ EL L V+ + LRAQ HE+ N+++ +G +
Sbjct: 289 RYKLIDDDGDYGGKVASFQVRSDDLQELIHTLSEVQQYSQDLRAQTHEYTNKLVISGWLQ 348

Query: 370 AGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEKGVSLRINSDTL 429
G A +F+ + QS+ + +++ EK + IN +
Sbjct: 349 LGHTDKAKQFIHE-EVGKQOSYEKVLFEQISDSTIQAILIGKLSKASEKKIEFTINEGSH 407

Query: 430 ILGTVKDFE---DVATILGNLINNAIDAABAGEAPRWIELTLMDDADTLVISVADSGPG 485

I + PE + TI+GN+I+NA DA V + P+ I++ L D + LVI VAD+G G
Sbjct: 408 I--NYQWPEQMTAQLVTIIGNIIDNAFVAVNTDNP-K-IDIFLTDMGNDLVIEVADNGTG 464
Query: 486 I-PEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVEGV 544
I P D + G S + + G+G+ L + AL G I +G VF V
Sbjct: 465 ISPADYD---NIMKQGYSTKDGQNRGYGLAL-VQAALLELQG--FLEITANEPNGTVFIV 518
Query: 545 KLP 547
+P
Sbjct: 519 YIP 521

>gi|16759585|ref|NP_455202.1| sensor kinase DpiB [Salmonella enterica subsp. enter
Typhi]
gi|29142642|ref|NP_805984.1| sensor kinase DpiB [Salmonella enterica subsp. enter
Typhi Ty2]
gi|25298491|pir|AP0579 sensor kinase DpiB (EC 2.7.3.-) [imported] - Salmonella e
subsp. enterica serovar Typhi (strain CT18)
gi|16501877|emb|CAD05102.1| sensor kinase DpiB [Salmonella enterica subsp. enteri
Typhi]
gi|29138273|gb|AA069844.1| sensor kinase DpiB [Salmonella enterica subsp. enteric
Typhi Ty2]
Length = 553

Score = 144 bits (362), Expect = 5e-33
Identities = 145/547 (26%), Positives = 241/547 (44%), Gaps = 36/547 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76
+ F RI ++ + +VA + D + + A++ + +ASN I V
Sbjct: 16 LAFPLRIFLLILVVSFIVAALAQYLSASFEDYLASHVRDMANQAKIIASNDIIAAVK 75
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVIDGLGIRLSHPDEERLGEQVSTS 136
N + LA +A T +VVI D IRL HP+ E++G + +
Sbjct: 76 -----NRDYKRLA-----IIANKLQRGTDFDYVVI GDRHSIRLYHPNPEKIGYPMQFT 123
Query: 137 FEAAM-RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAA 195
A+ RGE G++G + RAK PIF + +V +G VS+G+ + S FL
Sbjct: 124 KPGALERGESYFITGKSGSIGMAMRAKTPIFDNEGNV-IGVVSIGYLVSKIDSWRLDFFLLP 182
Query: 196 LALISVLGILIGVGVMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
+A + VL +++ + + R LG++P+++ +V+ Q A+ + EG++A+ P G
Sbjct: 183 MAGVFVLLLVLMLLSWFFAAHRRQMLGMEPKQIARVVRQOEALFSSVYEGLIAVDPEG 242
Query: 256 TIGVHNEQAQSMIGAGPMSGRT----LKEXXXXXXXXXXXXXHGQHPETVAH-NGRILYL 309
I N A+ M+G P GR + E + + +A+ NG +
Sbjct: 243 HITAINRNARKMLGL-PSPGRQWLGLKIAEVVNPADFFTCQIAERRQDVMANFNGLSVIA 301
Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ +R G++ LG +++ R + +I L+ +L ++ +LR RHE N + T GL+
Sbjct: 302 NREAIRSGEELLGAIISFRSKDEIATLNAQLTQIKQYVESLRTL RHEHLNWMSTLNGLLQ 361
Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGS--AHLNEXXXXXXXXXXXXXXKGVSLRI--N 425
E + S+ Q LI S + E G+ + I
Sbjct: 362 MKEYDRVREMVGESQAQQQ---LIDSLRGAFADRQVAGLLFGKVQRARELGLKMVIVPG 418
Query: 426 SDTLILGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDADTLVISVADSGP 484
S L D + A I+GNL++NA +A++ E IEL L D+ D +VI VAD G
Sbjct: 419 SQLHQLPEGLDSTEFAAIVGNLLDNAFEASLRTOEGDNTIELFLSDEGDEVVIEVADQGC 478

Query: 485 GIPEGV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVF 542
G+PE + +F E E HGIGL L + GG V ++ G +F
Sbjct: 479 GVPEALREKIFEQGVSTRADEPGE---HGIGLYLIASYVGRCCG-VITLEDNDPCGTLF 533

Query: 543 GVKLPGV 549
+ LP V
Sbjct: 534 SLFLPKV 540

>gi|28898486|ref|NP_798091.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
gi|28806704|dbj|BAC59975.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
Length = 539

Score = 141 bits (355), Expect = 4e-32
Identities = 142/548 (25%), Positives = 244/548 (44%), Gaps = 36/548 (6%)

Query: 17 IRFATRILVIQVATVALVVAICTGI-FAVLMMQMKTEAHTALSIGRSVASNPQIREEV 75
I F R+LVI + + + + F L ++Q + E AL + R +A + E+
Sbjct: 6 ISFRKRMLVIMTSLGLIELLLLVAAGFTYLVNQ-EHEMGEKALGVARFLAES-----EI 59

Query: 76 ALDTQTGANPSAEELADGDIQAVAQAANERTGALFVVI TDGLGIRLSHPDEERLGEQVS- 134
++ P Q +A + GA F+VI D G+RL HP +ER+G+ +
Sbjct: 60 VIEMVEAQQPEP-----YQESFRALTKAIGAAFIVIGDNQGVRLIHPVDERIGKPMKG 112

Query: 135 -TSFEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFL 193
+ A + G+ ++ G+LG S R K IF ++ +G VSVG+ D + R+ FL
Sbjct: 113 GDNQRALVEGQSYVSTARGSLGYSVRGKAAIFDAQNI-IGVSVGYLLDRLQDRIEPL 171

Query: 194 AALALISVLGILIGVGVAMGMRWRVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSP 253
A L L+ V+ ++ V+ R+++R LG +PEE+ L + I EGV++
Sbjct: 172 AFLILMVVVVVANAVVSNYASRKFRAILGFEPPEEIGRLYGELEVTMTSTIKEGVLSIDA 231

Query: 254 NGTIGVHNEQAQSMIGA--GPMSGRTLKEXXXXXXXXXXXXXXHQ--HPETVAHNGRILYL 309
G + N A ++G + L + GQ H + N + L
Sbjct: 232 QGVLRISINRSACQILGIDRDKALNKPLTDTLRSDLYTVLETGQEDHDIEIFLNHKRLIA 291

Query: 310 DFHPVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLID 369
+ P+ + +G V + R R +I EL+E+L + LR+Q HE N+++T +GL+
Sbjct: 292 NRSPIFVEGKIVGAVSSFRRLRDEINELTEQLSQTKEYADLLRSQTHEHRNKLNTISGLVQ 351

Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTL 429
G + + +G + + Q+ + + E G+ L + +
Sbjct: 352 MGELEAVQKLIGQETAH-YQAMIEFLRDTIKDPLIAGMLLGKTERARELGLQLVVEGSR 410

Query: 430 I--LGTVKDPEDVATILGNLINNAIDAAVA-----GEAPRWIELTLMDDADTLVISV 479
+ L + ED+ TILGNLI+NA DA ++ R IE+++ D + +++ V
Sbjct: 411 LEPLTEWLNSDLVTILGNLIDNAFDATLSVIRDESNVASERRNIEVSVSDYGNEVILEV 470

Query: 480 ADSGPGIFEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDG 539
+D G G+PE ++ T + G+GL L LA + G V ++ T G
Sbjct: 471 SDHGCGLPENIE---PQTLFKKGISTKSRQNRGVGLHLVNQLATRYHGHVEMLP-NTGHG 526

Query: 540 AVFGVKLP 547
V LP
Sbjct: 527 TRITVYLP 534

>gi|28211194|ref|NP_782138.1| sensor kinase dpiB [Clostridium tetani E88]

gi|28203634|gb|AA036075.1| sensor kinase dpiB [Clostridium tetani E88]
Length = 538

Score = 140 bits (352), Expect = 8e-32
Identities = 124/533 (23%), Positives = 251/533 (47%), Gaps = 52/533 (9%)

Query: 18 RFATRILVIQVATVALVVAICTGIFAVLMMQMK---TEAHTALSIGRSVASNPQIRE 73
+ RI V + LV+ I I L +M+ E AL + +++A +I+
Sbjct: 8 KITLRKIVTLYVFILVMVI--SIIGYLSFKEMRELIEKERSKEALRLAQTLMATDEIKR 65

Query: 74 EVALDTQTGANPSAEELADGDIQAVAQAANERTGALEFVVITDGLGIRLSHPDEERLGEQV 133
+ + + LA +Q + +T F+V+ D G R SHP EE +G+ +
Sbjct: 66 NLN-----KKDSLA---LQYYVERVRLKTNVTFIVVIDMEGTRYSHPIEENIGKMI 113

Query: 134 STS--FEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSV---YS 187
E G+ ++ GTLG S R P++ + G VSVG + +V Y+
Sbjct: 114 KGGDHIEVINSQSQSYVSESVCTGLSIRGFAPVYKDGEQI--GAVSVGILKGNVNLEVYN 171

Query: 188 RLPFMFLAALALISVLGILIGVGVAMGMRWRERVTLGLQPEELVTLVQNQTAVIDGIDEG 247
+L F+ * ++G++ G+ A + + GL+P+E+ L+ + A+++ +++G
Sbjct: 172 KLSKFIPIFI---LVGLITGILGAYLLAHSIKNSIYGLEPKETALLSLKEAILESVEDG 227

Query: 248 VLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXX---HGQHP---ETV 300
++A+ +G I +N+ A++++G +S R L + + + P E
Sbjct: 228 IIAVDKSGNINLYNKSANLLG---ISKRDLGKSVLNLYMPDESILEVLNTKKPLINVENK 284

Query: 301 AHNGRILYLDHFHPVRGDDQD-LGYVVTIRDRTDIELSERLDSVRTMTALRAQRHEFAN 359
+ G L +++ + D++ +G V+T D T I EL+E L V+ + +LRAQ HEF N
Sbjct: 285 INVGTTLMCNINILEDNRDKNFMGLVITFEDLTSIKELAEELTGVKILWSLRAQNHEFMN 344

Query: 360 RIHTATGLIDAGRVHDAEFLGDIS-RNGGQSHPLIGSAHLNXXXXXXXXXXXXXKEK 418
++HT +GLI +++ +++ + GG S+ + + ++ E+
Sbjct: 345 KLHTISGLIQIEEYDMVVDYICELAYKRGGISYLI--NENIKIIPLOGLLLAKYNKCEEE 402

Query: 419 GVSLRINSDTLI--LGTVKDPEDVATILGNLINNAIDA AVAGEAPRWIELTLMDDADTLV 476
+S I T + L + E++ +++GNL++N+++ AV + IE+ + ++ L
Sbjct: 403 KISFIKESTFLERLPNKMNSEEICSVVGNLVDNSME-AVEVDGTGKIEIEIRNNDKELF 461

Query: 477 ISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDV 529
+ V D+G GIP+ ++ +I E + + G+G+ + + + G++
Sbjct: 462 LMKDNGGGGIPKEIE-----EKIFLKEKSTKLGNRGLGMYIVKNIIEDKFGZI 509

>gi|23100675|ref|NP_694142.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
gi|22778909|dbj|BAC15176.1| two-component sensor histidine kinase [Oceanobacillus
HTE831]
Length = 533

Score = 136 bits (343), Expect = 9e-31
Identities = 135/543 (24%), Positives = 244/543 (44%), Gaps = 39/543 (7%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMM---DQMKTEAHTALSIGRSVASNPQIREEVA 76
TR+ ++ V LVV I +L+ +++K E A+ I R++A + +
Sbjct: 6 TRLSILITLVCLVVIIVLITNDLLINYATGERLKENIEKAVIISRTMAKSEWV----- 60

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALEFVVITDGLGIRLSHPDEERLGEQVSTS 136
G EE IQ + T F+V+ D GIR SHP+ E +G+
Sbjct: 61 ---INGLQNKDEEKY---IQEYTNIEISRYTDLTFIVVMDMDGIRKSHPNPELIGKPFVGG 114

Query: 137 FEAAM--RGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
E + +G E ++ GTLG S RA PIF + +G VSVG + +
Sbjct: 115 DEDTVLEQGIHISISEGTLGDSLRAFSPIFNEEGE-QIGAVSVGISLQEIDDVINNNHI 173

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
+ + S++G++IG+ A + R +R+ GL+P ++ L++ ++A ++ EG++ + +
Sbjct: 174 SNLISSIVGLIIGILGAWFIARYIKRILFGLPEFFQIAKLLKERSATLESAREGIITIDKD 233

Query: 255 GTIGVHNEQAQSMIGAGPMS----GRTLKEXXXXXXXXXXXXXXHGQHPETVAH--NGRILY 308
I + N+ A + ++ G+ ++E Q V NG +
Sbjct: 234 HKITIVNKAAMKVFEKAGITESPVGKNVEEVLPHSHLEDILKSKQPEMDVEQKINGVTIL 293

Query: 309 LDFHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLI 368
+ P+ D+ +G + T RD T++ +L+++L V+ ALRAQ HEF N++H G++
Sbjct: 294 ANRMPPIIVNDEVVGAISTFRDLTELKQLAKQLSGVKLYAEALRAQSHEFMNKLHVINGMV 353

Query: 369 DAGRVHDAAEFLGDI--SRNGCQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSLRINS 426
+ +++ I RN +H + ++ + E+ V+L+I+
Sbjct: 354 TTKSYDELDDYIKQIVNQRNDELNHVV--KNVKDSILAGFLLGKLSDARERDVNLQIDV 410

Query: 427 DTLILGTVKDP--EDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGP 484
I + + + TI+GNL +NAID A+ + R I++ + D L I + D G
Sbjct: 411 AEEIPASADNQVVHKLITIIGNLTDNAID-AIKSKENRTIDMYVSYKNDWLYIGIQDYGI 469

Query: 485 GIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARASHGGDVWVIDRGTEGAVFGV 544
GI E + Q+ + + + G GL L R + GG + E G +F V
Sbjct: 470 GIDEHIQ-----QQMFQKGYSTKGNNRGYGLYLVRQSVETLGGSLRF--ETLEAGTIFEV 522

Query: 545 KLP 547
++P
Sbjct: 523 EVP 525

>gi|15641613|ref|NP_231245.1| sensor kinase citA, putative [Vibrio cholerae O1 bio
N16961]
gi|11277516|pir|D82180 probable sensor kinase citA VC1605 [imported] - Vibrio ch
(strain N16961 serogroup O1)
gi|9656116|qb|AAF94759.1| sensor kinase citA, putative [Vibrio cholerae O1 biovar
N16961]
Length = 538

Score = 131 bits (329), Expect = 4e-29
Identities = 138/541 (25%), Positives = 236/541 (43%), Gaps = 56/541 (10%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMQMKTEAHTALSIGRSVASNPQIREEVA 76
I F R+L+I + + + + + E AL + +A P + +
Sbjct: 6 ITFRKRMLIIMTSLGLIELLLLVAAGFMYVKHSQEQQEVGQKALGVAFLAQTPAVINMI- 64

Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134
+TG A D Q + + GA F+VI D GIRL HP +ER+G+ +
Sbjct: 65 ---KTGR-----ASDDQQQSYRELTQLIGA AFIVIGDNQGIRLVHPIDERIGKPMVGG 114

Query: 135 TSFEAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
+ A + GE +++ G+LG S R K + + +G VSVG+ + + R+ FL
Sbjct: 115 DNERALVEGEAYVSFAQGS LGKSVRGKAAVVDQHGQI-IGVVS VGYLIERLQDRVEPFLE 173

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
L ++L + V+ RR++R LG +PEE+ L + + EG++++

Sbjct: 174 YLIATALLVVGANALVSSYASRRFQRAILGFEPPEIARLYVELDVTMSTLKEGIISIDDK 233

Query: 255 GTIGVHNEQAQSMIGAGPMSGRITLKEXXXXXXXXXXXXXHGQHPETVAHNGRI-----LYL 309
G + N+ A ++G L+ TV GR LYL

Sbjct: 234 GILRSINKSACEILG-----LRREQALNRRLTTILPESDLYTVLATGRTDHDIELYL 285

Query: 310 DFH-----FVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTHALRAQRHEFANRIH 362
+ H P+ + +G V + R R +I EL+E+L R LR+Q HE N+++

Sbjct: 286 NKHWIIANRSPIVEGKVVGAUSSFRLRDEINELTEQLAQTREYAEMLRSTHEHRNKLN 345

Query: 363 TATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNXXXXXXXXXXXXXXXXXKEGVSL 422
T +GL+ G + + +G + H + L E E+ L

Sbjct: 346 TISGLLQMGELDAVQQLIQETE-----HYQVLIEFLRETIKDPLIAGMLLGKTERAREL 400

Query: 423 RIN---SDTLILGTVK---DPEDVATILGNLINNAIDA---AVAGEAP-----RWIELTL 468
+ D L T+ EDV TILGNLI+NA +A A+ +P R IE+++

Sbjct: 401 GLELMVEDGARLETLPPIHKAEDVVITILGNLIDNAFEATLTARTLSPVPPERRVIEVSI 460

Query: 469 MDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHGIGLKLCLARASHGGD 528
D + +++ V D G G+P+ ++ + T+ G S ++ G+GL L + LA + G

Sbjct: 461 SDFGNEIILEVDDQGCGLPKELEHWQL-TEKGS--SKAVQNRGVGLFLVKQLADRYQCQ 517

Query: 529 V 529
+

Sbjct: 518 L 518

>gi|23112843|ref|ZP 00098276.1| COG3290: Signal transduction histidine kinase regu
citrate/malate metabolism [Desulfitobacterium hafniense]
Length = 458

Score = 131 bits (329), Expect = 4e-29
Identities = 119/461 (25%), Positives = 217/461 (47%), Gaps = 18/461 (3%)

Query: 95 IQAVAQAANERTGALFVITDGLGIRLSHPDEERLGEQVSTSFEA-AMRGEETMAWETGT 153
IQ +A+ TG ++VI D IR SHP +R+G + E +++ +E ++ G

Sbjct: 2 IQPLAERIRLATGVEYIVIFDMEKIRYSHPYLDRIGTVFNDGDEELSLQRKEYLSQAVGV 61

Query: 154 LGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG 213
+G S RA VP+ A + + VG V+VG ++ + L ++G+ +G +

Sbjct: 62 VGPSIRAFVPLADEGTRQVGVAVGILVPTIREIVGAIRVELYSSILIGLALGGLGSFY 121

Query: 214 MRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPM 273
+ ++ L+P ++ +++ + A+ +D+GV+AL I V NE+A + G

Sbjct: 122 LASNIKKNMFSLEBPSQIARMLSERVAIFQAMDDGVVALDMENRITVINEKACRIAGTSEK 181

Query: 274 S-GRTLKEXXXXXXXXXXXXXH--GQHPETVAHNGRILYLDHFHPVRRGDQDLGYVVTIRD 329
+ G L+E + E + +N +L +DF P+R +Q +G VVT+++

Sbjct: 182 AVGCPLQEFFAFTALSDFLETHDPAESTELILNNTWVL-VDELPIRVKEQVVGRRVTLKE 240

Query: 330 RTDIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQ 389
+T++ +++E L V+T ALR Q HE N +HT GLI + A E++ ++ +

Sbjct: 241 KTEVRKMAEELTGKTFIEALRVQNHESLNTLHTIAGLIQLDKADQAMEYIYRVTEEQE 300

Query: 390 SHPLIGSAHLNXXXXXXXXXXXXXXXXXKEGVSLRINSDTLI--LGTVKDPEDVATILGNL 447
+ S+ + E V + + D+ + L D + ILGNL

Sbjct: 301 VTKFL-SSKIMYPNVAGLLLKGYNRGKELKVDVLPDSRLSELPEGFDSNTLTIIILGNL 359

Query: 448 INNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNER 507

+ NA++A V + + + + L++SV D+GPGI A Q+ + +
 Sbjct: 360 LENAMEAVVGSKISE-VHCRIKHEHHQLILSVEDTGPGIS-----LANQAQMYQWGFSTK 413

Query: 508 THGH-GIGLKLCLARSHGGDVWVIDRGTEGAVFGVKLP 547

+G+ GIGL L + GG + + + G FGV++P
 Sbjct: 414 GNGNRGIGLSLVKQTVDLLGGTIEM--ETGKWGTRFGVRIP 452

>gi|18309513|ref|NP_561447.1| two-component sensor histidine kinase [Clostridium p
 gi|18144190|dbj|BA980237.1| two-component sensor histidine kinase [Clostridium pe
 13]
 Length = 516

Score = 130 bits (326), Expect = 9e-29

Identities = 116/515 (22%), Positives = 230/515 (44%), Gaps = 43/515 (8%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVA 76

++F +IL+ + + +A+ +F + M + +T S++ P I+E++
 Sbjct: 3 VKFENKILLWAILITFIPLALSFTLFIEDKLSYMDSDVRNTLKETAFSISEIPFIQEDL- 61

Query: 77 LDTQTGANPSAELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134

+ N +E I+A+ +V+ D G++ SH DE+++G+
 Sbjct: 62 --SNGEINSRIQEYTKHFIEAINDVD-----IIVVADMRGVKYSHLDEKQIGQVFN 112

Query: 135 TSFRAAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194

E +G + G++G + R P+ + VG + VG Y+ + + L
 Sbjct: 113 DKKEVLTQSSSYSLMKGSMGETLRWFQPVMY--NGKQVGFIMVG---KYYNEIQL-LT 165

Query: 195 ALALISVLGI-----LIGVGVAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVL 249

LI +G+ LI + ++ R+ ++ LG++PEE+ L + + +++ + EG++
 Sbjct: 166 HKTLIKYMGFLFVLITILISKLFARKVKKAILGMEPEETIAALYKEKKIILNTVSEGII 225

Query: 250 ALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEXXXXXXXXXXXXXXGQHPETVAHNGRILYL 309

AL+ N I N+ +I G + LK+ + + G+ +++
 Sbjct: 226 ALNKNNEITEINDNCYKLID-GFSKYKVLKLLPYIEENKPVEMKE---IILQGKKV 280

Query: 310 DFHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTALRAQRHEFANRIHTATGLID 369

P+ + + LG V+T+ DR DI +++ + V + LRA HEF N +H GLI
 Sbjct: 281 TIQPIMKKG EYLGSVITLMDRNDIRKIAKEITGVDEVVKNLRANVHEFRNNLHVILGLIQ 340

Query: 370 AGRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXGKVSRLRNSDTL 429

G +A +++ + + + +++ + E+GV+ + ++
 Sbjct: 341 LGEYEEARKYI--LKTQKIHENNSLKFSNVEDYYVRGLLLSRELVAKERGVNFILTEESF 398

Query: 430 ILGTVK--DPEDVATILGNLINNAIDAAVAGEAP-RWIELTLMDDADTLVISVADSGPGI 486

+ G D D+ TILGNLI NA D+ V + +E+TL +D + + + V D+G I
 Sbjct: 399 LFGNHNYVDSYDIVTILGNLIENAFDSCVCSSENKEVEVTLYEDDEKIQVRDNGKPI 458

Query: 487 PEGVD--VFATATQIGDSEDNERTHGHGIGLKLCL 519

+ +F ++G S E G G GL L +
 Sbjct: 459 DNNIKERIF----ELGVSSKGE---GRGTGLSLVK 486

>gi|16077825|ref|NP_388639.1| two-component sensor histidine kinase [Bacillus subt
 gi|21362406|sp|Q34427|CITS_BACSU Sensor protein citS
 gi|7428877|pir|E69600 two-component sensor histidine kinase citS - Bacillus subt
 gi|2443240|dbj|BA922311.1| yf1R [Bacillus subtilis]
 gi|2633082|emb|CAB12587.1| two-component sensor histidine kinase [Bacillus subtil

subtilis str. 168]
Length = 542

Score = 128 bits (321), Expect = 3e-28
Identities = 137/538 (25%), Positives = 240/538 (44%), Gaps = 35/538 (6%)

Query: 21 TRILVIQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASNPQIREEVALDTQ 80
T+I+ + A + V+ + T AV + +AE A+ R+++ P ++E +
Sbjct: 12 TKIMGLIAALLVFGVIGVLTITLAVQHTQGERRQAEQLAVQTARTISYMPVVKELI----- 66

Query: 81 TGANPSAEELADG---DIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSF 137
E DG Q V + E+TGA + + + G S + L +++ S
Sbjct: 67 -----ERKDGHAQTQEVIEQMKEQTGAFAIYVLNEKGDIRSASGKSGL-KKLSRSR 117

Query: 138 EAAMRGEETMAWETGTLGASA-RAKVPIFAPDS--SVPVGEVSVGFERDSVYSRLPMFLA 194
E G ET G R PI S +G VSV F + + L
Sbjct: 118 EILFGGSHVS--ETKADGRRVIRGSAPIIKEQKGYSVQVIGSVSVDFLOTETEQSIKKHLR 175

Query: 195 ALALISVLGILIGVGVAMGMRRRRWERVTGLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
L++I+VL +L+G A + + + TLGL+P E+ L + + A++ I EG++A +
Sbjct: 176 NLSVIAVLVLLLCFIGAAVLAKSIRKDTLGLLEPHEIAALYRERNAMLFAIREGIIATNRE 235

Query: 255 GTIGVHNEQAQSMIG-AGPMSGRTLKEXXXXXXXXXXXXXXGQH--PETVAHNCRILYLD 311
G + + N A M+ P+ + + G+ + V+ N ++ ++
Sbjct: 236 GVVTTMNVSAAEMLKLPEFVIHLPIDDVMPGAGLMSVLEKGEMLPNQEVSVNDQVFIINT 295

Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
+ +G Q G VV+ R++T++ +L + L VR + LRAQ HEF+N+++ GL++ G
Sbjct: 296 KVMNQGGQAYGIVVSFREKTELKKLIDTLTEVRKYSEDLRAQTHBFSNKLIALGLLELG 355

Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRI--NSDTL 429
+A + + + + H L+ +++ EK V L I NS
Sbjct: 356 EYDEAIDLIKEYAIQNEQHDLLFH-NIHSQQVQAILLGKISKASEKKVKLVIDENSSLA 414

Query: 430 ILGTVKDPEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGPIEG 489
L + TI+GNLI+NA + AVA ++ + + + D +VI V+D+GPG+P
Sbjct: 415 PLPAHIGLSHLITIIGNLIDNAFE-AVAEQSVKEVLFFITDMGHDIVIEVSDTGPQVPP- 472

Query: 490 VDVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ + G S R G GL + R GG + + ++ T GAVF V +P
Sbjct: 473 -EKIEAVFERGYSSKGMR--RGYGLANVKDSVRELGGWIELANQKT-GGAVFTVFIP 525

>gi|21398531|ref|NP_654516.1| HATPase_c, Histidine kinase-like ATPases [Bacillus a
gi|30260733|ref|NP_843110.1| sensory box histidine kinase [Bacillus anthracis str
gi|30254182|gb|AAP24596.1| sensory box histidine kinase [Bacillus anthracis str.
Length = 534

Score = 127 bits (318), Expect = 8e-28
Identities = 107/412 (25%), Positives = 191/412 (46%), Gaps = 31/412 (7%)

Query: 95 IQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSF EA-AMRGEETMAWETGT 153
IQ + TG F+V+ D GIR SHP+ +++G E A++G+E ++ GT
Sbjct: 75 IQTYTNRILKNTGVQFIVVMDMNGIRKSHPNPQKIGHHFIGGDEGPALKGKEHVSLAECT 134

Query: 154 LGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG 213
LG S R VPIF+ ++ +G V+VG D+V R+ + + +G+L+G+ A+
Sbjct: 135 LGISM RVFVPIFS-ETGEQLGAVAVGISADNVKERVKESRHIIYIGVGVGVLVGIIGAIL 193

Query: 214 MRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGP- 272
+ R ++ GL+P + +++ + ++ + EG++A+ + + N +A+ +
Sbjct: 194 LARHIKKSLEFGLPHRIAKILEERNTMLQSVKEGIIAVDKARVTLINNEAKRLFKKSGL 253

Query: 273 -----MSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVRRGDQD 320
M +KE + T+ N LY+ ++
Sbjct: 254 EEDFIGKDOVELYMPNSRIKEVLQTGEVQLNEEQNIYGITIVTNRVPLYVK-----EEI 306

Query: 321 LGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFL 380
+G + T RD+T+I +L+E L +R ALRAQ HEF N++H GL + + ++
Sbjct: 307 VGAIATFRDKTEIRKLAELTGIRLYAEALRAQSHEFMNKMHVVLGLTHMKQYEELQKY- 365

Query: 381 GDISRNGGQSHPLIGSA--HLNEXXXXXXXXXXXXXXKEGVSLRINSDTLI--LGTVKD 436
IS + IG + EK + L I+ D+ + +
Sbjct: 366 --ISGMVSEHQYEIGGVMKRIKSPVFAGFLLGKLSYAREKNIKLIISEDSYMPEIDDESI 423

Query: 437 PEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
++ TI+GNLI+NA++A E R +E+ + + D L I+V D+G GI E
Sbjct: 424 THELITIVGNLIDNALEAVTNCEKKR-VEVKIQHE-DILTITVQDTGKGIIQE 473

>gi|30018763|ref|NP_830394.1| Two-component sensor kinase yufl [Bacillus cereus AT
gi|29894304|gb|AAP07595.1| Two-component sensor kinase yufl [Bacillus cereus ATCC
Length = 534

Score = 125 bits (314), Expect = 2e-27
Identities = 107/412 (25%), Positives = 189/412 (45%), Gaps = 31/412 (7%)

Query: 95 IQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSFEE-AMRGEETMAWETGT 153
IQ + TG F+V+ D GIR SHP+ +++G E A++G+E ++ GT
Sbjct: 75 IQTYTNRILONTGVQFIVVMDMNGIRKSHPNPQKIGHHFIGGDEGPALKGKEHVSLAEGT 134

Query: 154 LGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMG 213
LG S R VPIF+ ++ +G V+VG D+V R+ + + +G+L+G+ A+
Sbjct: 135 LGISMRVFPVPIFS-ETGEQLGAVAVGISADNVKERVKESRHIIYIGVGVGVVLVGIIGAIL 193

Query: 214 MRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGP- 272
+ R ++ GL+P + +++ + ++ + EG++A+ + + N +A+ +
Sbjct: 194 LARHIKKSLEFGLPHRIAKILEERNTMLQSVKEGIIAVDKARVTLINNEAKRLFKKSGL 253

Query: 273 -----MSGRTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDHFHVRRGDQD 320
M +KE + T+ N LY+ +
Sbjct: 254 EEDFIGKDOVELYMPNSRIKEVLQTGEVQLNEEQNIYGITIVTNRVPLYVK-----GEI 306

Query: 321 LGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFL 380
+G + T RD+T+I +L+E L +R ALRAQ HEF N++H GL + + ++
Sbjct: 307 VGAIATFRDKTEIRKLAELTGIRLYAEALRAQSHEFMNKMHVVLGLTHMKQYEELQKY- 365

Query: 381 GDISRNGGQSHPLIGSA--HLNEXXXXXXXXXXXXXXKEGVSLRINSDTLI--LGTVKD 436
IS + IG + EK + L I+ D+ + +
Sbjct: 366 --ISGMVSEHQYEIGGVMKRIKSPVFAGFLLGKLSYAREKNIKLIISEDSYMPEIDDESI 423

Query: 437 PEDVATILGNLINNAIDAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
++ TI+GNLI+NA++A E R +E+ + D L I+V D+G GI E
Sbjct: 424 THELITIVGNLIDNALEAVTNCEKKR-VEVKI-QHGDILTITVQDTGKGIIQE 473

>gi|23007702|ref|ZP_00049454.1| COG3290: Signal transduction histidine kinase regu

citrate/malate metabolism [Magnetospirillum
magnetotacticum]
Length = 279

Score = 124 bits (310), Expect = 6e-27
Identities = 95/279 (34%), Positives = 139/279 (49%), Gaps = 17/279 (6%)

Query: 110 FVVITDGLGIRLSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGASARAKVPFAPDS 169
+VV+TD G+R SHPD R+GE+VST + GE +TGTLG S R KVP+F P+
Sbjct: 1 YVVVTDDGVRYSHPDPTRIGERVSTDPVPLSGEVWTGTQTGTLGESWRVKVPVFGPEG 60

Query: 170 SVPVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRRWERVTLGLQPEE 229
V VG SVG + L L L + +GV A + R R L+PEE
Sbjct: 61 DV-VGTASVGILESDLADDLADDLGWLLAALSVAALGVVCAAFVTRAVRRRIFRLEPEE 119

Query: 230 LVTLVQNQTAVIDGIDGVLALSPNGTIGVHNEQAQSMIG--AGPMSGRTLKEXXXXXXX 287
+ L++ + A++ GI EGV+AL +G + + N++AQ ++G A GR +
Sbjct: 120 IGRLLLETRDAMLHGISEGVVALDRDGA VVLVNDEAQRLLGIAAADAVGRPAHDVLDLPQLL 179

Query: 288 XXXXXHGQH-----PET----VAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDI 333
+ FE V R+L R + +G V+ +RD T++
Sbjct: 180 ALVPDTAETADDADAPAAGPEEGALVLAGERVLLARADRARDVGRVGTVLLLRDHTL 239

Query: 334 IELSERLDSVRTMTTHALRAQRHEFANRIHTATGLIDAGR 372
L LD R +T ALRAQ HEFAN++H +GL++ G+
Sbjct: 240 HALLRDLGDARGLTDALRAQSHEFANKLHVVSGLLELGQ 278

>gi|16077512|ref|NP_388326.1| similar to two-component sensor histidine kinase [Yd
subtilis]
gi|15213974|sp|P96601|DCTS_BACSU Probable C4-dicarboxylate sensor kinase
gi|7428876|pir|A69771 two-component sensor histidine kinase homolog ydbF - Bacil
subtilis
gi|1881255|dbj|BAA19282.1| PROBABLE SENSORY TRANSDUCTION HISTIDINE KINASE. [Bacil
gi|2632745|emb|CAB12252.1| two-component sensor histidine kinase [Bacillus subtil
subtilis str. 168]
Length = 535

Score = 117 bits (293), Expect = 6e-25
Identities = 125/508 (24%), Positives = 214/508 (42%), Gaps = 37/508 (7%)

Query: 53 EAEHTALSIGRSVASNPQIREEVALDTQTGANPSAEELADGDIQAVAQAANERTGALFVW 112
E + ++ R+V+ +++E +A QT A A E +I+ + +A ++V
Sbjct: 42 BLKKRLMNTARTVSEMTEVKEALARKKQTEAVRHAVE-----BIRMINBAD-----YIV 90

Query: 113 ITDGLGIRLSHPDEERLGEQVSTSFEEAMRGEETMAWET-GTLGASARAKVPFAPDSSV 171
+ D IR +HP +G++ + E A E E G +G + RA P+ D +
Sbjct: 91 VMDMNHIRYTHPVSTSIGKKSEGADEEAFAEHIYPSEAKGEIGTAVRAFYPVKDQDLN- 149

Query: 172 PVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRRWERVTLGLQPEELV 231
+G V VG + L +A I VL + G+ + + R ++ L+P E+V
Sbjct: 150 QIGVVLVGKTLPGIADILLHLKRDI AFIVLTLGFGLAGSFLARHIKKQMFQLEPHEIV 209

Query: 232 TLVQNQTAVIDGIDGVLALSPNGTIGVHNEQAQSMIGA-GPMSGRTLKEXXXXXXXXXXXXX 290
+ + +TA ++EGV+A+ I + NE+A+ + G + G+ + E
Sbjct: 210 RMYEERTATFHSNNEGVIADNRLVITIFNEKAKQIFEVQGD LIGKVIWEVLKDSRLPEI 269

Query: 291 XXHGQ--HPETVAHNGRILYLD FHPVRRGDQDLGYVVTIRDRTDIELSERLDSVRTMTTH 348
+ + E + +G+++ P+ + +G V +DRT+ +++E L VR

Sbjct: 270 VERNKAVYNEEIRVSGKVIMSSRIPIVMKKKVIGAVAIFQDRTEAAKMABELTGVRNFVE 329

Query: 349 ALRAQRHEFANRIHTATGLIDAGRVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXX 408
ALR Q HE N++HT GLI G+ A + S + + N+

Sbjct: 330 ALRVQNHEHMKLHTIAGLIQLGKSEKALQLAFQASTEQENVTEFLHRSIQND-AAAGLL 388

Query: 409 XXXXXXXXKEKGVSLRI--NSDTLILGTVKOPEDVATILGNLINNAIDA--AVAGEAPRWI 464
E G+++ I NS D D+ +LGNLI NA + V E R I

Sbjct: 389 LSKIRRGRELGIHAVHIDENSSLQQFPFHVVDQHDIVVLLGNLIENAFGSFETVQSEDKR-I 447

Query: 465 ELTLMDDADTLVISVADSGPGI-----PEGVDVFATATQIGDSEDNERTHGHGIGLKLCR 519
++++ D L I + D+G GI P D T + G G G GL L +

Sbjct: 448 DISIEQTDLDLAILIEDNGCGIEPTHMPRLYDKGFTVNKTG-----GTGYGLYLVK 498

Query: 520 ALARSHGGDVWVIDRGTEDGAVFGVKLP 547
+ G + V D G F + P

Sbjct: 499 QIIDKSGGTIEV-DSHAGQGTSTFSIVFP 525

>gi|29375782|ref|NP_814936.1| sensory box histidine kinase [Enterococcus faecalis
gi|29343243|gb|AA081006.1| sensory box histidine kinase [Enterococcus faecalis v5
Length = 516

Score = 116 bits (291), Expect = 9e-25
Identities = 89/371 (23%), Positives = 174/371 (46%), Gaps = 33/371 (8%)

Query: 25 VIQVATVALVVAICTGIFAVLMMDQMKTEAHTALSIGRSVASNPQIREEVALDTQTGAN 84
VI +AT+ +++ G+ V + +++ E L++G +A P + E + D +

Sbjct: 13 VIFIATLIIMITFFYGVTTVQTIKEVRKNQEALLAVGEQLAIEPNVIEALKNDHYS--- 69

Query: 85 PSABELADGDIQAVAQAANERTGAL---FVVITDGLGIRLSHPDEERLGEQVSTSFEA- 139
+EL +A R G + F+VI + GIRL+HPD +++G+ E

Sbjct: 70 ---DEL-----EAYTVRLGEIHQLDFIVIMNMQGIRLTHPDRQKIGKHFEGGDEV 117

Query: 140 AMRGEETMAWETGTGLGASARAKVPIFAPDSSVPVGEVSVGFERDSV--YSRLPMFLAAL 196
A++GEE ++ G+LG S R VP++ D +G V++G + S+ R

Sbjct: 118 ALKGEHLSVSQGSLSLGRGFVPVY--DQKQIGVVAMGIKMTSLSQLIERTKNDYTVS 175

Query: 197 ALISV-LGILIGVGVAMGMRWRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNG 255
L+SV G ++ + V+ ++++ L+P E+ L++ + A+++ + +L + +

Sbjct: 176 VLLSVGFGFILAIVVSYYLKKQLH---DLEPREIARLLEERNAMLEETKDAILVIDTDQ 231

Query: 256 TIGVHNEQAQSMIGAGPMSGRTL---KEXXXXXXXXXXXXXXGQHQPETVAHNIRILYLD 312
I + N +A M S L K H + + NG+ ++

Sbjct: 232 NILLANIEATKMYHNITNSEENLLGKKLSALVLSPEKLVVHSKTEQFYRQNGQDYFVSIA 291

Query: 313 PVRRGDQDLGYVVTIRDRDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGR 372
P+ + +G+V+ +++ T+ ++E+L S T AL++Q HEF N++H GL+D

Sbjct: 292 PINVRKKTIGHVIFLKNATETTFIVAEQLVSTTTYASALQSQSHEFMNKMHVIVGLVDLED 351

Query: 373 VHDAAEFLGDI 383
+L D+

Sbjct: 352 YEALKHYLADL 362

>gi|15615315|ref|NP_243618.1| two-component sensor histidine kinase [Bacillus halo
gi|15213978|sp|Q9K997|DCTS_BACMD Probable C4-dicarboxylate sensor kinase
gi|25298483|pir|H83993 two-component sensor histidine kinase BH2752 [imported] -

halodurans (strain C-125)
gi|10175373|dbj|BAB06471.1| two-component sensor histidine kinase [Bacillus halodurans]
Length = 532

Score = 115 bits (288), Expect = 2e-24
Identities = 114/450 (25%), Positives = 197/450 (43%), Gaps = 24/450 (5%)

Query: 110 FVVITDGLGIRLSHPDEERLGEQVSTSFEEAMRGEETMAWETGTLGA-SARAKVPIFAPD 168
++V+ + IR++HP ERL E E + T G + RA +PI
Sbjct: 91 YIVLLNMDRIRITHPIPERLQTPFVGQDEDPAFAEHIYLSKAKTEGVVTVRAFMPILNQ 150
Query: 169 SSVFVGEVSVGFERDSVYSRLPMFLAALALISVLGILIGVGVAMCMRRRWERTLGLQPE 228
VG VG S + F LI ++ L G + + +R T ++P+
Sbjct: 151 RE-QVGVAVVGSVLPSTYADMIQEFWQPALIGLITALEFGFWGSWLLASHIKRQTFNMEPD 209
Query: 229 ELVTLVQNQTAVIDGIDBGVLALSPNGTIGVHNEQAQSMIGAGPMS-GRTLKEXXXXXXX 287
EL L+ + A + I EGV+A++ + I + NE A+ M+G + GR + E
Sbjct: 210 ELAHLVERDASFNAIHEGVVAINKHEKITIMNEAARRMLGVKEKAIGRNIHEVIPDTKL 269
Query: 288 XXXXXHGO--HPETVAHNGRILYLDHFVRRGDQDLGVVVTIRDRTDIELSERLDSVRT 345
G+ + GR+++ + P++ + +G + +D++D+ L+E L V+
Sbjct: 270 PEILSIGKPLYQREFYIQGRLVFSNRIPQIDGETVGAIAIFQDKSDVDRLAELTGVQA 329
Query: 346 MTHALRAQRHEFANRIHTATGLIDAGRVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXX 405
ALR Q HE++N++HT GLI A +++ D+ + ++ ++
Sbjct: 330 FVDALRVQNHEYSNKLHTIAGLIQLDEGKKALQYIFDLLEEQEFGVGV-MQKIHNDSL 388
Query: 406 XXXXXXXXXXXXKEGVSLRINSDTLILGTVKDPEDVAT-----ILGNLINNAIDA-AVAGE 459
E GV + I D+ + PE V T I+GNLI+N++DA + +
Sbjct: 389 GLLLGKVSRLGKELGVQVIEKDESEF---IDHPEGVTTHDLVVIVGNLIDNSLDAFSSTQD 445
Query: 460 APRWIELTLMDDADTLVISVADSGPGIPEGV--DVFATATQIGDSEDNERTHGHGIGLKL 517
+ + + + ++ D L I V D+G GI E V +F + T G GIGL L
Sbjct: 446 QNKTVHVFEGEENDFLKIRVRDNGEGIREEVREKMFVRGFS-----TKSTSGRGIGLPL 499
Query: 518 CRALARSHGGDVWVIDRGTEGAVFGVKLP 547
+A+ G + V + G F + LP
Sbjct: 500 IQAIVERVEGKIEV-ESELNIGTTFSIYLP 528

>gi|21398509|ref|NP_654494.1| hypothetical protein predicted by GeneMark [Bacillus
A2012]
Length = 260

Score = 110 bits (276), Expect = 6e-23
Identities = 69/255 (27%), Positives = 143/255 (56%), Gaps = 14/255 (5%)

Query: 17 IRFATRILVIQVATVALVVAICTGIFAVLMMDQMKTEAEHTALSIGRSVASNPQIREVA 76
++ RI + A + +V+ + + +F ++ + ++ + AL + ++VA+ P+I+E A
Sbjct: 6 LKLQPRITLTISALILVVLMLTSYLFYILSETVEEQIGKRALHVAKTVAAIPEIK--A 63
Query: 77 LDTQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV--S 134
T+ NP++ IQ +A+ T A F+V+ + GIR +HP+ ++GE +
Sbjct: 64 FQTE---NPAS-----IIQPIAERIRMDTEADFIVGNKEGIRYAHPERDKIGEAMIGG 114
Query: 135 TSFEAMRGEETMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLA 194
+ + G+ ++ TG+LG S R KVPI ++ + +G VSVGF D ++ + ++
Sbjct: 115 DNKGVLLEGKSYVSKATGSLGPSLRGKVPIRQENEI-IGVSVSGFSMDDIHGAVEVYGK 173

Query: 195 ALALISVLGILIGVGVAMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPN 254
+ I+++G+LIGV ++ + +R+ G++PEE+ +L + + VI + EG++ + N
Sbjct: 174 RVFWITIIIGLLIGVIGSIYLAGSIKRMFMGMEPEEISSLYEEHSTVIQSVREGIIVIDQN 233

Query: 255 GTIGVHNEQAQSMIG 269
G I + N+ A ++
Sbjct: 234 GMISLVNQAAYDILA 248

>gi|28900618|ref|NP_800273.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
gi|28808998|dbj|BAC62106.1| putative sensor kinase Cita [Vibrio parahaemolyticus]
Length = 524

Score = 110 bits (275), Expect = 7e-23
Identities = 104/435 (23%), Positives = 192/435 (44%), Gaps = 12/435 (2%)

Query: 98 VAQAANERTGALFVVITDGLGIRLSHPDEERLGEQV-STSFEEAMR-GEETMAWETGTLG 155
+ A + A F+ ++D GIRL+HP ER+G V E A+ GE +++ G+LG
Sbjct: 75 IINAVQAVSDADFITVSDRAGIRLAHPVAERVGLPVLGGDIERALENGESYLSYGVGSLG 134

Query: 156 ASARAKVPIFAPDSSVPVGEVSVGFERDSVYSLPMFLAALALISVLGILIGVGVAMGMR 215
S R PIF+ + V +G + VG+ D++ L L ++ + I + ++
Sbjct: 135 PSVRYISPIFSNEG DV-IGMIKVGYLIDTLDLWTSERLPLISFGIIAIVAICTWLSWKFS 193

Query: 216 RRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSG 275
R L+P +L ++ V+ EG++A++ G++ + N+ A++M+ G
Sbjct: 194 RYVRTQMQLPEPWLKQALKTHQGVLOATYEGVLVAINSEGSLYLINDSARAMLNHYHQELG 253

Query: 276 RTLKEXXXXXXXXXXXXXXHGQHPETVAHNGRILYLDLDFHPVRRGD-QDLGYVVTIRDRTDII 334
+ + NG+ L ++ +R + G V ++RD+ ++
Sbjct: 254 NVFTDGIDNPESFSLKGDDYINGLIRVNGKNLVMNRVTLRTSTGEPYGAVFSLRDQNMH 313

Query: 335 ELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFLGDISRNGGQSHPLI 394
LSE++ V +R RHE+ N++ T +GL+ G +D A + QS
Sbjct: 314 VLSEKISQVTQYMNMRVARHEYQNKLTISGLLQMG-AYDKALSVCLSQAKASQSQLDS 372

Query: 395 GSAHLNEXXXXXXXXXXXXXXKEGVSLRIN--SDTLILGTVKDPEDVATILGNLNNAI 452
A + E GV+L I+ SD L E + ++GNL NA+
Sbjct: 373 LHALNSRPALSALILAKASKANELGVALSIDCQSDLSALSRRLSEEQLCGLIGNLAQNAL 432

Query: 453 DAAVAGEAPRWIELTLMDDADTLVISVADSGPGIPEGVDVFATATQIGDSEDNERTHGHG 512
+ AV G+ + + + A I V+++GP + DV ++G + + HG
Sbjct: 433 E-AVKGQENGHVHIGISESACEYTIQVSNNGPLLESEFDVLC---ELGFTTKQNKAD-HG 487

Query: 513 IGLKLCRALARSHGG 527
+G+ L R++ G
Sbjct: 488 VGMVLRVRSIVEQGNG 502

>gi|29140597|ref|NP_803939.1| sensor kinase Cita [Salmonella enterica subsp. enter
Typhi Ty2]
gi|29136221|gb|AAO67788.1| sensor kinase Cita [Salmonella enterica subsp. enteric
Typhi Ty2]
Length = 539

Score = 107 bits (268), Expect = 5e-22
Identities = 123/545 (22%), Positives = 238/545 (43%), Gaps = 33/545 (6%)

Query: 19 FATRILVIQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASNPQIREEVALD 78
F RI ++ + T +V+ T + +++ + AL +++ P++ E V
Sbjct: 15 FQNRIFLLILFTSTIVMLAITWYLTDTIKERLHYQVGQRALIQAMQISAMPELVEAV--- 71

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136
A +L+ I+A+ + A ++ + + G RL H + + +G+ + S
Sbjct: 72 -----EAHDLR--IKALIDPMRSFSDATYITVGNEKGQRLYHVPDEIGKYMEGGDS 122

Query: 137 FEAAMRGESTMAWETGTLGASARAKVPIFAPDSSVPVGEVSVGFERDSVYSRLPMFLAAL 196
+A + ++ G+LG+S R K PI V +G VSVG+ + + S L + +++L
Sbjct: 123 DDALYNAKSYSVSRKGSLSGSSLRGKSPIQDSTGKV-IGIVSVGYTLEQLESWNLQISSL 181

Query: 197 ALISVLGILIGVGVAMGMRRRWERVTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256
+ +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +
Sbjct: 182 LFPMAILLVLLYCARRFSLHIKKQMLNMEPQQLSQLLIQQSVLFESVFEGLIAIDSHHR 241

Query: 257 IGVHNEQAQSMIG-AGPMS---GRTLKEXXXXXXXXXXXXXH-GQHPETVAHNGRILYLD 311
I N+ A+ ++ + P S G + + E V N +
Sbjct: 242 ITAINQTARLLNLSQPESELIGYAIHHIVLPEAFFXDAPQKNKKDEIVTFNQMKVIASR 301

Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
V +Q G+V++ R++ DI L+ +L VR LRA +HE N I T GL+
Sbjct: 302 MAVIIDNQPGWVISFRNKDDINTLNLQLSQVRQYADNLRAVQHEHRNLSTIAGLLFLK 361

Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKGVSLRINSDTLI- 430
R +A + S + + I S + + E G+ L + + +
Sbjct: 362 RYDNALALIQQSESHQKVLDPI-SHNFRDHHLAGLLIGKYRAKELGLELIFDPSSFVE 420

Query: 431 -LGTVKDPEDVATILGNLINNAIDAAGV-EAPRWIELTLMDDADTLVISVADSGPGIPE 488
L + + +I+GNL++NA +A + E R IE + + + ++I VAD G GI E
Sbjct: 421 HLPSSLSHNEWISIVGNLLDNAYNATLLNREGSRQIECLINSEGNEVIEVADQGCIDE 480

Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKL 546
+ +F ++ D HGIGL L + + GD+ ++D G +F + +
Sbjct: 481 NIRQHIFERGVTTHNGD-----HGIGLWLVS YVKQANGDI-IVDNNNSFGTIFTLYI 533

Query: 547 PGVME 551
P E
Sbjct: 534 PFTR 538

>gi|16759047|ref|NP_454664.1| sensor kinase cita [Salmonella enterica subsp. enter Typhi]
gi|25298488|pir|AH0508 sensor kinase cita (EC 2.7.3.-) [imported] - Salmonella e subsp. enterica serovar Typhi (strain CT18)
gi|16501337|emb|CAD01208.1| sensor kinase cita [Salmonella enterica subsp. enteri Typhi]
Length = 539

Score = 107 bits (267), Expect = 6e-22

Identities = 123/545 (22%), Positives = 238/545 (43%), Gaps = 33/545 (6%)

Query: 19 FATRILVIQVATVALVVAICTGIFAVLMMDQMKEAHTALSIGRSVASNPQIREEVALD 78
F RI ++ + T +V+ T + +++ + AL +++ P++ E V
Sbjct: 15 FQNRIFLLILFTSTIVMLAITWYLTDTIKERLHYQVGQRALIQAMQISAMPELVEAV--- 71

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136
A +L+ I+A+ + A ++ + + G RL H + + +G+ + S
Sbjct: 72 -----EAHDLR--IKALIDPMRSFSDATYITVGNEKGQRLYHVPDEIGKYMEGGDS 122

Query: 137 FEAAMRGEETMAWETGTLGASARAKVPFAPDSSVPVGEVSVGFERDSVYSRLPMFLAAL 196
+A + ++ G+LG+S R K PI V +G VSVG+ + + S L + +++L
Sbjct: 123 DDALYNAKSYVSVRKGSLSGSSLRGKSPIQDSTGKV-IGIVSVGYTLEQLESWLNQISSL 181

Query: 197 ALISVLGILIGVGVAMGMRRRWERVTGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256
+ +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +
Sbjct: 182 LFPMAILLVLLYCARRFSLHIKKQMLNMEPQQLSOLLIQSVLFESVFEGLIAIDSHR 241

Query: 257 IGVHNEQAQSMIG-AGPMS---GRTLKEXXXXXXXXXXXXXH-GQHPETVAHNGRILYLD 311
I N+ A+ ++ + P S G + + E V N +
Sbjct: 242 ITAINQTARLLNLSQPESELIGYAIHHIVLPEAFFYDAPQKNKKDEIVTFNQMKVIASR 301

Query: 312 HPVRRGDQDLGXVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
V +Q G+V++ R++ DI L+ +L VR LRA +HE N I T GL+
Sbjct: 302 MAVIIDNQPGQWVISFRNKDDINTLNLQLSQVRQYADNLRAVQHEHRNLSTIAGLLFLK 361

Query: 372 RVHDAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEKGVSLRINSDTLI- 430
R +A + S + + I S + + E G+ L + + +
Sbjct: 362 RYDNALALIQQQSESHQKVLDFI-SHNFDRDHLAGLLIGKYRAKELGLELIFDPSSFVE 420

Query: 431 -LGTVKDPEDVATILGNLINNAIDAAGVAG-BAPRWIELTLMDDADTLVISVADSGPGIPE 488
L + + +I+CNL++NA +A + E R IE + + + ++I VAD G GI E
Sbjct: 421 HLPSSLSHNEWISIVGNLLDNAYNATLLNREGSRQIECLINSEGNEVIIIEVADQCGIDE 480

Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARALSHGGDVWVIDRGTEDGAVFGVKL 546
+ +F ++ D HGIGL L + + GD+ ++D G +F + +
Sbjct: 481 NIRQHIFERGVTTHNNGD-----HGIGLWLVSYSYVKQANGDI-IVDNNNSFGTIFTLYI 533

Query: 547 PGVME 551
P E
Sbjct: 534 PFTRZ 538

>gi|1705888|sp|P52687|CITA_KLEPN Sensor kinase cita
gi|2126138|pir||S70538 signal-transducing histidine kinase cita - Klebsiella pneu
gi|924991|gb|AAC44733.1| sensor kinase Cita
Length = 547

Score = 106 bits (265), Expect = 1e-21

Identities = 120/541 (22%), Positives = 236/541 (43%), Gaps = 33/541 (6%)

Query: 19 PATRILVIQVATVALVVAICTGIFAVLMMDQMKTAEHTALSIGRSVASNPQIREEVALD 78
F RI ++ + T +V+ + + + + AL +++ P++ E V
Sbjct: 20 FQNRIFLLILFTSTIVMLAMSWYLTLDITEERLHYQVGQRALIQAMQISAMPELVEAV--- 76

Query: 79 TQTGANPSAEELADGDIOAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136
+LA I+A+ + A ++ + D G RL H + + +G+ + S
Sbjct: 77 -----QKRDAR--IKALIDPMRSFSDATYITVGDAQRLYHVPDEIGKSMEGGDS 127

Query: 137 FEAAMRGEETMAWETGTLGASARAKVPFAPDSSVPVGEVSVGFERDSVYSRLPMFLAAL 196
EA + + ++ G+LG+S R K PI V +G VSVG+ + + + L + +++L
Sbjct: 128 DEALINAKSYVSVRKGSLSGSSLRGKSPIQDATGKV-IGIVSVGYTIEQLENWLSLQISSL 186

Query: 197 ALISVLGILIGVGVAMGMRRRWERVTGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256
+ + +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +
Sbjct: 187 LIPMAIMLLLLLFCARRFSLHIKKQMLNMEPQQLSOLLIQSVLFESVFEGLIAIDSDYK 246

Query: 257 IGVHNEQAQSMIGAG----PMSGRTLKEXXXXXXXXXXXXXH-GQHPETVAHNGRILYLD 311

I N+ A+ ++ + G+ + + E V N +
 Sbjct: 247 ITAINQTARRLLNLSQPEPTLIGKRISVISQEVFFYDAPQTNKKDEIVTFNQIKVIASR 306
 Query: 312 HPVRRGDQDLGYVVTIRDRTDIIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371
 V ++ G+V++ R + DI LS +L V+ LRA +HE N I T GL+
 Sbjct: 307 MAVILNNEPQGWVISFRSKDDINTLSLQLSQVQYADNLRAVQHEHRNLSTIAGLLFLK 366
 Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXKEGVSRLRINSDTLI- 430
 R + A E + S + + I + + + E G+ L + + +
 Sbjct: 367 RYNQALELIQQQSESHQKVIDFI-ARNFQDNHLAGLLIGKYYRAKELGLELIFDPACFVD 425
 Query: 431 -LGTVKDPEDVATILGNLINNAIDAAV-AGEAPRWIELTLMDDADTLVISVADSGPGIPE 488
 L T + +I+GNL++NA +A++ + + IE + D ++I +AD G GI E
 Sbjct: 426 RLPTALSHNEWISIVGNLLDNAYNASLRQPQGSQIECLINSDGQEVIIIEIADQCGGIDE 485
 Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARSHGGDVWVIDRGTEGAVFGVKL 546
 + +F S+D HGIGL L R+ GG + V++ G +F + +
 Sbjct: 486 ALRDRIFERGVTSSASKD-----HGIGLWLVRSYVEQAGGSI-VVENNIPFGTIFTLYI 538
 Query: 547 P 547
 P
 Sbjct: 539 P 539

>gi|27366560|ref|NP_762087.1| Signal transduction histidine kinase regulating citr
 metabolism [Vibrio vulnificus CMCP6]
 gi|27358126|gb|AA007077.1| Signal transduction histidine kinase regulating citrat
 metabolism [Vibrio vulnificus CMCP6]
 Length = 519

Score = 104 bits (260), Expect = 4e-21
 Identities = 99/428 (23%), Positives = 194/428 (45%), Gaps = 15/428 (3%)

Query: 106 TGALFVVITDGLGIRLSHPDEERLG-EQVSTSFEEAAMR-GEETMAWETGTLGASARAKVP 163
 + A F+ ++D GIRL+HP ER+G V + A+ GE ++ G+LG S R P
 Sbjct: 80 SDADFITVSDEEGIRLAHPVSEVRGLPVVGGDIQRALNLGEAYLSQSVGSLGPSVRYISP 139
 Query: 164 IFAPDSSVPVGEVSVGF--ERDSVYSRLPMFLAALALISVLGILIGVGVAMGMRRRWERV 221
 IF+P+ V VG V VG+ E +++SR + L L +V + + + ++ ++
 Sbjct: 140 IFSPEGEV-VGMVKVGYLVETLNLWSREKLL--PLLLFAVSALSFLLLSWRFSSYVKKQ 196
 Query: 222 TLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGTIGVHNEQAQSMIGAGPMSGRTLKEX 281
 L+P +L ++ V+D E V+A++ G I + N+ A++++ + G+ K+
 Sbjct: 197 MQDLEPWQLKQALKTHQGVLDATHEAVAVNQGNINYLANDAARAILRQSELVGKETKQL 256
 Query: 282 XXXXXXXXXXXXHGQHPETVAHNGRILYLDHFVRRGD-QDLGYVVTIRDRTDIIELSERL 340
 + + ++ +R + + G V T+R R+++ LS+R+
 Sbjct: 257 DDASHLFHLDGDDFLDKVAQLGSDGVIINRVMTRTSNGEAGAVFTLRRSELQALSDRI 316
 Query: 341 DSVRTMTHALRAQRHEFANRIHTATGLIDAGRVHDAAEF-LGDISRNGGQSHPLIGSAHL 399
 V ++R HE N++ +GL+ G A L ++N + L G +
 Sbjct: 317 SQVDKYLESMRVTHHEHQNKLSVISGLLQMGAFDKALSVCLAQAQONQTRIDSLQGVKSM 376
 Query: 400 NEXXXXXXXXXXXXXXXXXXKEGVSRLRINSDTLILGTVKDPEDVATILGNLINNAIDAAVAGE 459
 + + +++ D L E V +++GNLI+N ++A G+
 Sbjct: 377 PQLTALLAKLSKARESNQSLNIACYGDLGSLTQRVSEQVCSLVGNLIDNGLEAC-QGQ 435
 Query: 460 APRWIELTLMDDADTLVISVADSGPGIPEGVDFATATQIGDSEDNERTHGHGIGLKLCL 519
 + + L + + +++ +GP + E ++ S E HGIGL L +

Sbjct: 436 NDAIMVVKLRETEEEFILTFSSNNGPSLDEEDLESICRWGYSTKSATGE---HGIGLHLVK 491

Query: 520 A-LARSHG 526

+ L+ +HG

Sbjct: 492 SILSRAHG 499

>gi|16763443|ref|NP_459058.1| putative transcriptional regulator [Salmonella typhi]
gi|16418548|gb|AA19017.1| putative transcription regulator [Salmonella typhimuri]
Length = 539

Score = 103 bits (256), Expect = 1e-20

Identities = 125/545 (22%), Positives = 238/545 (43%), Gaps = 33/545 (6%)

Query: 19 FATRILVIOVATVALVVAICTGIFAVLMDQMKTEARHTALSIGRSVASNPQIREEVALD 78

F RI ++ + T +V+ T + +++ + AL +++ P++ E V

Sbjct: 15 FQNRIFLLILEFTSTIVMLAITWYLTDPITKERLHYQVGQRALIQAMQISAMPELVEAV--- 71

Query: 79 TQTGANPSAEELADGDIQAVAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVS--TS 136

A +L+ I+A+ + A ++ + + G RL H + + +G+ + S

Sbjct: 72 -----EAHDLR--IKALIDPMRSFSDATYITVGNEKGQRLYHVNPFDEIGKYMEGCDS 122

Query: 137 FEAMARGEETMAWETGTLGASARAKVPFAPDSSVFGVSVGFERDSVYSRLPMFLAAL 196

+A + ++ G+LG+S R K PI V +G VSVG+ + + S L + +++L

Sbjct: 123 DDALYNKASYVSVRKGLGSSLRGKSPIQDSTGKV-IGIVSVGYTLEQLESWLNLIQISSL 181

Query: 197 ALISVLGILIGVGVMGMRRRWERTLGLQPEELVTLVQNQTAVIDGIDEGVLALSPNGT 256

L +L+ + A ++ L ++P++L L+ Q+ + + + EG++A+ +

Sbjct: 182 LFPMALLLLVLVLYCARRFSLHIKKQMLNMFQQLSQLLIQQSVLPFESVFEGLIAIDSHHR 241

Query: 257 IGVHNEQAQSMIG-AGPMS---GRTLKEXXXXXXXXXXXXXX-H-GQHPETVAHNGRILYLD 311

I N+ A+ ++ + P S G + + E V N +

Sbjct: 242 ITAINQTARRLLNLSQPESELIGYAIHHVVLPEAFFYDAPQKNKKDEIVTFNQMKVIASR 301

Query: 312 HPVRRGDQDLGYVVTIRDRDITIELSERLDSVRTMTHALRAQRHEFANRIHTATGLIDAG 371

V +Q G+V++ R++ DI LS +L VR LRA +HE N I T GL+

Sbjct: 302 MAVIIDNQPGQWVISFRNKDDINTLSLQLSQVROYADNLRVQHEHRNLISTIAGLLFLK 361

Query: 372 RVHDAAEFLGDISRNGGQSHPLIGSAHLNEXXXXXXXXXXXXXXXXXXEGVSLRINSDTLI- 430

R +A + S + + I S + + E G+ L + + +

Sbjct: 362 RYDNALALIQQQSESHQKVLDFI-SHNPFRDHHLAGLLIGKYRAKELGLELIFDPSSFVE 420

Query: 431 -LGTVKDPEDVATILGNLNNDAIDAAVAG-EAPRWIELTLMDDADTLVISVADSGPGIFE 488

L + + +I+GNL++NA +A + E R IE + + + ++I VAD G GI E

Sbjct: 421 HLPSSSLSHNEWISIVGNLLDNAYNATLLNREGSRQIECLINSEGNEVIIEVADQCGIDE 480

Query: 489 GV--DVFATATQIGDSEDNERTHGHGIGLKLCLARLARSHGGDVWVIDRGTEDGAVFGVKL 546

+ +F ++ D HGIGL L + + GD+ ++D G +F + +

Sbjct: 481 NIRQHIFERGVTTTHNNGD-----HGIGLWLVHSYVKQANGDI-IVDNNNPFGTIFTLYI 533

Query: 547 PGVME 551

P E

Sbjct: 534 PFTRE 538

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF
Posted date: Jan 14, 2004 12:40 AM
Number of letters in database: 528,039,549
Number of sequences in database: 1,605,642

Lambda	K	H
0.317	0.135	0.386

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 51,380,962
Number of Sequences: 1605642
Number of extensions: 2020487
Number of successful extensions: 5969
Number of sequences better than 10.0: 273
Number of HSP's better than 10.0 without gapping: 20
Number of HSP's successfully gapped in prelim test: 253
Number of HSP's that attempted gapping in prelim test: 5749
Number of HSP's gapped (non-prelim): 305
length of query: 551
length of database: 528,039,549
effective HSP length: 130
effective length of query: 421
effective length of database: 319,306,089
effective search space: 134427863469
effective search space used: 134427863469
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 76 (33.9 bits)